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(54) **METHOD FOR PREPARING WATER SOLUBLE POLYPEPTIDES**  
VERFAHREN ZUR HERSTELLUNG VON WASSERLÖSLICHEN POLYPEPTIDEN  
PROCEDE DE PREPARATION DE POLYPEPTIDES SOLUBLES DANS L'EAU

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- **PROCEEDINGS OF THE NATL. ACADEMY OF SCIENCES USA, vol. 85, November 1988, Washington, DC (US); P.F. BRAY et al., pp. 8683-8687**
- **ANNUAL REVIEWS OF CELL BIOLOGY, vol. 3, 1987, Annual Reviews Inc.; C.A. BUCK, pp. 179-205**
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## Description

[0001] This invention is concerned with the preparation of complex soluble receptors. In particular it is directed to the synthesis of recombinant receptors for cell matrix or plasma proteins.

[0002] Cellular membranes contain polypeptides which are lodged in the lipid bilayer. Such polypeptides contain a domain which anchors the protein in the cell membrane, a hydrophobic transmembrane domain, together in many instances with a C-terminal cytoplasmic sequence. In general, these polypeptides are single chain molecules or are multiple chain molecules derived from an ancestral single chain expression product by post-translational proteolytic processing. Such multiple chain polypeptides usually are covalently linked by disulfide bonds. However, some of these polypeptides are noncovalently associated with one another by salt bridges, Van der Waals forces, hydrophobic interactions and the like, and in such cases this association of polypeptide subunits into a larger aggregate is a prerequisite for biological activity.

[0003] The biological activity of such membrane-bound, multiple subunit molecules is varied, but in general reflects a receptor or binding function. Receptors serve to signal the cell regarding a condition or substance in the exterior environment of the cell, they serve to internalize an extracellular substance, or they function to attach cells to one another, to extracellular matrix substances, cell surface or plasma proteins.

[0004] A further subclass of membrane bound multiple subunit polypeptides are those in which each subunit is different, i.e. is not substantially homologous, and is encoded by a discrete gene. Such polypeptides are termed "MSP" (multiple subunit polypeptides) for the purposes of this invention. Numerous examples of such polypeptides or receptors are known, but the most substantial group is the class of cell surface receptors for extracellular matrix molecules, some of which have currently been identified and DNA encoding them cloned (see for example, Buck et al., "Ann. Rev. Cell Biol." 3:179 [1987] and Ruoslahti et al., "Science" 238: 491 [1987].)

[0005] Of particular interest is the platelet glycoprotein IIb-IIIa, a platelet membrane-bound receptor involved in platelet aggregation and which binds to fibrinogen, fibronectin, vitronectin and von Willebrand factor. The two subunits constituting this receptor have been cloned (Fitzgerald et al. "Biochemistry" 26:8158 [1987] and Fitzgerald et al. "J. Biol. Chem." 262(9):3936 [1987]). Bennett et al. reported expression of the GPIIb subunit in Cos-1 cells, but the subunit was not found on the cell membrane (AHA 61st Scientific Sessions, Nov. 15, 1988). Bennett et al. suggested that membrane localization might require the formation of the IIb-IIIa complex. There was no teaching or suggestion that a recombinant, membrane-bound GPIIb-IIIa, even if it could be made, would bind to its proper ligands, e.g., fibrinogen. In addition, an oral disclosure by Frelinger *et al.* at the same meeting purported to describe the transient expression of full length GPIIb-IIIa on an unidentified recombinant cell surface; no other information was provided relating to the manner in which expression was allegedly obtained.

[0006] European patent application EP-A-244267 describes the production of a decay accelerating factor (DAF) amino acid sequence variant in which a predetermined amino acid residue or polypeptide is inserted into, deleted from or substituted, for an amino acid residue or polypeptide of the native mature or pre-DAF amino acid sequence.

[0007] International application WO 89/00200 describes a nucleic acid sequence defining a structural gene coding for a portion of the hGPIIb protein.

[0008] Work has previously been performed on immunoglobulin T-cell receptor gene fusions in which a chimeric gene construct containing a T-cell receptor  $\alpha$ -chain variable domain and the constant region coding sequences of an immunoglobulin  $\alpha$ 2a molecule have been formed (Gascoigne N.R.J et al. Proc. Natl. Acad. Sci. USA, Vol 84 pp 2936-2940 May 1987).

[0009] Bennett, J. S. et al. determined that GP11b, once glycosylated and cleaved was not inserted into the plasma membrane. They deduced that this process may therefore require prior formation of a GPIIb/IIIa complex. (1234, Circulation Supplement - Abstracts from the 61st scientific sessions, Art 11; Vol 78, No. 4 October 1988).

[0010] Corbi *et al.* orally reported the transient expression of functional full length LFA-1 in COS cells in September 1988 at the Titisee Symposium sponsored by Boehringer Ingelheim.

[0011] Membrane-bound MSPs present difficulties in purification and stability since the hydrophobic domains tend to induce the MSPs to micelles or aggregates. A form of these receptors is needed that is soluble, particularly in body fluids such as blood and in pharmacological excipients such as saline, without forming multiple molecular aggregates beyond proper heterodimer assembly. Accordingly, it is an object herein to synthesize such MSP forms.

[0012] It is another object to produce soluble forms of the GPIIb-IIIa receptor which are capable of properly binding their normal ligands.

[0013] It is a further object to express GPIIIa in recombinant cell culture.

[0014] It is an additional object to produce high yields of GPIIb-IIIa from recombinant cell culture.

[0015] These and other objects will be apparent from consideration of this application as a whole.

[0016] In accordance with this invention, a method is provided for the preparation of a soluble analogue of an integrin comprising an  $\alpha$ -subunit and a  $\beta$ -subunit, comprising:

(1) introducing into the nucleic acid encoding the  $\alpha$ -subunit and the  $\beta$ -subunit of the integrin a mutation which serves to delete or modify the membrane anchor domains thereof such that the mutated nucleic acid encodes an amino acid sequence variant of the integrin which is no longer capable of becoming lodged in a cell membrane,  
 (2) transforming a host cell with the nucleic acid of step (1),  
 (3) culturing the host cell of step (2), and  
 (4) recovering from the host cell culture soluble integrin comprising associated  $\alpha$ - and  $\beta$ -subunits, said integrin being biologically active as demonstrated by its ability to bind a ligand ordinarily bound by the integrin.

**[0017]** Also in accordance with this invention, an amino acid sequence variant of an integrin is provided in which the transmembrane domain of the integrin chain is modified so that it is no longer capable of becoming lodged in the cell membrane.

**[0018]** In an embodiment of the invention, the integrin is a heterodimeric receptor that participates directly in inter-cellular adhesion of cells to extracellular matrix proteins, for example, a leukocyte adhesion receptor or a member of the VLA family.

**[0019]** In a further embodiment the integrin is GPIIb-IIa, Mac1 LFA-1 or p150, 95.

**[0020]** The invention further provides a secreted amino acid sequence variant of an integrin which is biologically active as demonstrated by its ability to bind to a ligand ordinarily bound by the integrin, the variant comprising naturally associated  $\alpha$ - and  $\beta$ -subunit.

**[0021]** Also provided is a method for the preparation of GPIIb-IIIa comprising transforming a permissive host cell with nucleic acid encoding GPIIb-IIIa and culturing the host cell until GPIIb-IIIa accumulates in the cell membrane.

**[0022]** In particular embodiments a polypeptide comprising a biologically active extracellular domain of an integrin is fused at its C-terminus to an immunoglobulin constant domain, or is linked to an immunogenic polypeptide.

**[0023]** The MSP variants provided herein are purified and formulated in pharmacologically acceptable vehicles for diagnostic or preparatory utility or *in vivo* use in the modulation of cell adhesion.

**[0024]** Figs. 1a-1f depict the amino acid and nucleotide sequence of a secreted form of the GPIIb subunit of the MSP GPIIb-IIIa. The signal processing site for the heavy and light forms of this subunit are designated, respectively, with arrow-H and arrow-L.

**[0025]** Figs. 2a-2d depict the amino acid and nucleotide sequence of a secreted form of the GPIIIa subunit of the MSP GPIIb-IIIa. The signal processing site is designated with an arrow.

**[0026]** Fig. 3 depicts a comparison of the native and redesigned nucleic acid sequences at the 5' end of the GPIIIa gene.

**[0027]** An MSP is defined herein to be a multichain polypeptide, at least one chain of which is ordinarily anchored in a cell membrane and at least two chains of which are discretely encoded. MSPs ordinarily contain at least two distinct chains, two of which are lodged directly in the cell membrane. One or more additional chains may be covalently or noncovalently bound to the MSP chains ordinarily lodged in the cell membrane, but the additional chains may not themselves be anchored in the membrane. Such chains typically result from the post-translational processing of a single chain that becomes membrane anchored. Discretely encoded subunits are those which do not result from the posttranslational processing of a single translated protein, and their amino acid sequences are not homologous (i.e. the sequences of the subunits are not the same, and they do not assemble in nature into dimers or multimers of the same polypeptide). Instead, they are produced by the translation of independent mRNAs or polycistronic messages. Thus, the nucleic acids encoding MSP polypeptides ordinarily are found in nature under the control of different promoters and other transcription control sequences. MSPs include principally cell surface receptors for extracellular matrix molecules, also defined as cellular adhesion receptors. Many of these receptors and their ligands, such ligands including the extracellular matrix molecules and plasma proteins such as fibrinogen as well as cell surface proteins such as I-CAM, are central to cellular adhesion phenomena involved in wound healing, morphogenic mobility, developmentally unrelated cellular migrations, hemostasis and metastasis. These cellular adhesion receptors are identified by functional and structural features. Functionally, they typically bind to polypeptides incorporating the sequence RGD, from which they are dissociated by competition with other polypeptides containing the RGD sequence such as the peptides RGDS or RGDV. Also, they frequently require a divalent cation such as calcium for ligand binding. MSPs may or may not include members of the immunoglobulin superfamily such as the T cell receptor. A group of MSPs involved in cell surface intracellular adhesive interactions have been designated integrins (see Buck *et al.*, "Ann. Rev. Cell Biol." 3:179-205 [1987]).

**[0028]** Structurally, such cellular adhesion receptors belong to a supergene family of multimers in which a first single-chain polypeptide or disulfide cross-linked multi-chain polypeptide ( $\alpha$ -chain) is noncovalently associated with a second and different polypeptide (designated a  $\beta$ -chain), thereby forming a heteromultimer. The  $\alpha$ -chains of these receptors are quite diverse in terms of their amino acid sequence, and include the  $\alpha$  subunit of avian integrin (band 1);  $\alpha_1$ ,  $\alpha_2$ , and  $\alpha_4$  of VLA 1, 2 and 4;  $\alpha_3$  of VLA 3 and avian integrin (band 2);  $\alpha_F$  of VLA 5 and the fibronectin receptor;  $\alpha_L$  of LFA-1;  $\alpha_M$  of Mac-1;  $\alpha_x$  of p150,95;  $\alpha_H\alpha_L$  of GPIIb; and  $\alpha_v$  of vitronectin. The  $\beta$ -chains typically fall into three classes,  $\beta_1$

(avian integrin [band 3]; fibronectin receptor and VLA),  $\beta_2$  (LFA-1/Mac-1; p150,95) and  $\beta_3$  (GPIIb-IIIa and vitronectin receptor), the members of each  $\beta$ -class being substantially homologous or identical. It is preferred that the MSP selected contain the two (or more) chains which ordinarily associate with one another in nature since non-naturally occurring heteromers may not form complexes.

5 **[0029]** Each chain of an MSP is expressed in its native environment as a preprotein comprising a secretion signal which is processed during the extracellular orientation of the receptor. Also, at least one chain of each subunit will have a hydrophobic anchor containing a polypeptide sequence serving as a site for covalent addition of lipid, e.g. phospholipid, or a domain located in the C-terminal portion of the polypeptide and containing about from 10 to 30 predominantly hydrophobic residues such as phe, leu, ile, val, met, gly and ala. Such membrane anchoring sequences or domains  
10 will be collectively referred to herein as membrane anchor domains. A short hydrophilic cytoplasmic domain, on the order of 10 to 100 residues, usually is found C-terminal to transmembrane domains. The term subunit should be understood to mean polypeptide chain; it does not refer to domains or functional subregions of a given polypeptide chain.

15 **[0030]** Certain MSPs share other structural features, for example, wherein one subunit of the receptor contains cysteine-rich tandem amino acid sequence repeats in which greater than about 80% of the cysteine residues are alignable within about two residues of the cysteine residues of the tandem repeats of GPIIIa, wherein one subunit has the consensus N-terminal sequence Tyr/Phe/Leu-Asn-Leu-Asp, or one subunit contains an amino acid domain having substantial sequence homology to the calmodulin calcium binding site.

20 **[0031]** Also included within the scope of MSPs are those receptors which are homologous to the above-described members of the integrin superfamily. Homologous, as defined herein, means having the sequence of a polypeptide of a member of the integrin superfamily which at least has substantially the same amino acid sequence homology to a known member of the superfamily as any presently known member has to any other known member. Typically, homologous means having greater than about 40% amino acid homology after aligning sequences for maximum homology, but not taking into account conservative substitutions.

25 **[0032]** This invention in part is based upon the discovery that discretely encoded MSPs, when modified to eliminate their ability to insert into the host cell membrane, nonetheless are fully assembled and secreted in biologically active form by recombinant host cells. Recombinant host cells secrete the subunits in correct association with one another such that the assembly exhibits the biological activity of the extracellular domain of the native MSP, despite the fact that proper association of the subunits is no longer facilitated by juxtaposition in the cell membrane. Further, proper assembly has been obtained even when the MSP sequences have not been fused to multimer-forming polypeptides,  
30 i.e. it has been found that MSPs will properly associate even without the aid of extraneous cross-linking polypeptides such as immunoglobulin chains.

35 **[0033]** Biological activity is defined in terms of the ability of the secreted MSP to qualitatively bind the ligand ordinarily bound by the MSP in its native environment, although it will be appreciated that the kinetics or other quantitative characteristics of ligand binding by the secreted MSP may vary from those of the native cell bound MSP. While secreted MSP most likely will retain many functional immune epitopes capable of cross-reacting with antibody raised against the native MSP, this alone is not enough for the secreted MSP to exhibit biological activity as defined herein; "biologically active" secreted MSP must exhibit the ability to bind to its ligand as well. However, it will be understood that not all MSP produced in accord with this invention need to exhibit biological activity in the sense defined here. Such biologically inactive but, for example, immunologically active MSP analogues find use in diagnostic assays, in raising antibodies  
40 against MSP, or in the purification of antibodies to MSP.

45 **[0034]** This invention is particularly concerned with amino acid sequence variants of MSPs. Amino acid sequence variants of MSPs are prepared with various objectives in mind, including increasing the affinity of the MSP for its binding partner, facilitating the stability, purification and preparation of the MSP (including enhanced water solubility and reduced membrane affinity), increasing its plasma half life, improving therapeutic efficacy as described above, introducing additional functionalities and lessening the severity or occurrence of side effects during therapeutic use of the MSP. Amino acid sequence variants of MSPs fall into one or a combination of the following classes: insertional, substitutional or deletional variants. Each MSP variant or analogue will have one inactivated membrane anchor domain, and this will be accomplished by insertion, substitution or deletion, but these variants optionally comprise additional mutations that are involved in other than inactivating the membrane anchor domain of one chain of the native MSP.

50 **[0035]** Insertional amino acid sequence variants are those in which one or more amino acid residues extraneous to the MSP are introduced into a predetermined site in the MSP including the C or N termini. Such variants are referred to as fusions of the MSP and a polypeptide containing a sequence which is other than that which is normally found in the MSP at the inserted position. Several groups of fusions are contemplated herein.

55 **[0036]** Immunologically active MSP fusions comprise an MSP and a polypeptide containing a non-MSP epitope. The non-MSP epitope is any immunologically competent polypeptide, i.e., any polypeptide which is capable of eliciting an immune response in the animal to which the fusion is to be administered or which is capable of being bound by an antibody raised against the non-MSP polypeptide. Typical non-MSP epitopes will be those which are borne by allergens, autoimmune epitopes, or other potent immunogens or antigens recognized by pre-existing antibodies in the fusion

recipient, including bacterial polypeptides such as trpLE, beta-galactosidase, viral polypeptides such as herpes gD protein, and the like. Immunogenic fusions are produced by cross-linking *in vitro* or by recombinant cell culture transformed with DNA encoding an immunogenic polypeptide. It is preferable that the immunogenic fusion be one in which the immunogenic sequence is joined to or inserted into the MSP or fragment thereof by a peptide bond(s). These products therefore consist of a linear polypeptide chain containing MSP epitopes and at least one epitope foreign to the MSP. It will be understood that it is within the scope of this invention to introduce the epitopes anywhere within the MSP molecule or fragment thereof. Such fusions are conveniently made in recombinant host cells or by the use of bifunctional cross-linking agents. The use of a cross-linking agent to fuse the MSP to the immunogenic polypeptide is not as desirable as a linear fusion because the cross-linked products are not as easily synthesized in structurally homogeneous form.

**[0037]** These immunogenic insertions are particularly useful when formulated into a pharmacologically acceptable carrier and administered to a subject in order to raise antibodies against the MSP, which antibodies in turn are useful in diagnostics or in purification of MSP by immunoaffinity techniques known *per se*. Alternatively, in the purification of MSPs, binding partners for the fused non-MSP polypeptide, e.g. antibodies, receptors or ligands, are used to adsorb the fusion from impure admixtures, after which the fusion is eluted and, if desired, the MSP is recovered from the fusion, e.g. by enzymatic cleavage.

**[0038]** Other fusions, which may or may not also be immunologically active, include fusions of the mature MSP sequence with a signal sequence heterologous to the MSP, fusions of transmembrane-modified MSPs (including sequence deletions or modifications so that the MSP could not lodge in the cell membrane), for example, to polypeptides having enhanced plasma half life (ordinarily >about 20 hours) such as immunoglobulin chains or fragments thereof which confer enhanced plasma half life.

**[0039]** Signal sequence fusions are employed in order to more expeditiously direct the secretion of the MSP. The heterologous signal replaces the native MSP signal, and when the resulting fusion is recognized, i.e. processed and cleaved by the host cell, the MSP is secreted. Signals are selected based on the intended host cell, and may include bacterial yeast, mammalian and viral sequences. The native MSP signal or the herpes gD glycoprotein signal is suitable for use in mammalian expression systems.

**[0040]** Plasma proteins which have enhanced plasma half-life longer than that of soluble forms of MSPs having modified membrane anchor domains include serum albumin, immunoglobulins, apolipoproteins, and transferrin. Preferably, the MSP-plasma protein used for the fusion is not significantly immunogenic in the animal in which it is used (i.e., it is homologous to the therapeutic target) and the plasma protein does not cause undesirable side effects in patients by virtue of its normal biological activity.

**[0041]** In a specific embodiment the MSP extracellular domain is conjugated with an immunoglobulin constant region sequence. Immunoglobulins and certain variants thereof are known and many have been prepared in recombinant cell culture. For example, see U.S. Patent 4,745,055; EP 256,654; Faulkner *et al.*, *Nature* 298:286 (1982); EP 120,694; EP 125,023; Morrison, *J. Immun.* 123:793 (1979); Köhler *et al.*, *P.N.A.S. USA* 77:2197 (1980); Raso *et al.*, *Cancer Res.* 41:2073 (1981); Morrison *et al.*, *Ann. Rev. Immunol.* 2:239 (1984); Morrison, *Science* 229:1202 (1985); Morrison *et al.*, *P.N.A.S. USA* 81:6851 (1984); EP 255,694; EP 266,663; and WO 88/03559. Reassorted immunoglobulin chains also are known. See for example U.S. patent 4,444,878; WO 88/03565; and EP 68,763 and references cited therein. See also Gascoigne *et al.*, *P.N.A.S. USA* 84:2936-2940 (May, 1987), EP 325,224, and Thesis of Andrew Scott Peterson (Harvard University; degree awarded November 22, 1988).

**[0042]** Ordinarily, the extracellular domains of MSPs are fused C-terminally to the N-terminus of the constant region of an immunoglobulin in place of the variable region(s) thereof, retaining at least functionally active hinge, C<sub>H</sub>2 and C<sub>H</sub>3 domains of the constant region of an immunoglobulin heavy chain. Two forms of such fusions are embraced herein. In one, the extracellular domains of two or more ordinarily membrane-bound MSP chains are fused N or C terminally to immunoglobulin constant regions (heterofusion), while in the other form only one chain of the MSP is fused to a constant region (monofusion). The heterofusions include fusions with either light or heavy chain constant regions, or both. The heterofusion is produced by transforming a host cell with DNA encoding the light chain fusions, the heavy chain fusions or both. For example, transfection with DNA encoding one MSP chain fused to a heavy chain constant region and the other MSP chain fused to a light chain constant region will result in heterotetramers or heterodimers bearing light and heavy chain fusions with MSP chains. These are not as desirable as monofusions since they are not as likely to be biologically active. Note that monofusions may contain more than one fused chain, but in these cases the MSP chain will always originate with the same subunit.

**[0043]** Monofusions are immunoglobulin variants in which one chain of an MSP is fused to a heavy or light chain (or constant domain thereof), while the remaining chain(s) of the MSP are not fused to an immunoglobulin but rather are associated with the fused chain in substantially the fashion as is normally the case with the native MSP. Typically, both the fused and unfused MSP chains in monofusions will be variants in which the membrane anchor domains are modified so as to not lodge in the membrane, most commonly where the membrane anchor domain of one MSP chain is deleted, and in the other the membrane anchor domain is deleted and then the remaining extracellular region fused at its N-

terminus to the C-terminus of an immunoglobulin constant domain. The MSP chain or its fragment is fused to either a light chain or a heavy chain, but preferably a heavy chain. If the MSP only contained one membrane anchored chain then the remaining chain(s) will typically have their native sequence.

**[0044]** It may be desirable to produce mono-or polyfusions having immunoglobulin antigen binding capability as well as the capacity to bind the MSP ligand. Such products are made by transforming the host cells with DNA encoding light and heavy chain capable of binding an antigen (or are selected to already produce light chain) together with the light and/or heavy chain MSP fusion and the unfused MSP chain(s) (in the case of monofusions). This will yield constructs, for example, having the normal structures of immunoglobulins except that one or both light-heavy arms of the immunoglobulin will comprise a fusion with one chain of the MSP which in turn is assembled (covalently or noncovalently) with the remaining chain(s) of the MSP.

**[0045]** In those instances in which the fusion transformants also produce (or are transformed to produce) immunoglobulin chains not fused to an MSP subunit, the immunoglobulin variable domains may have unknown or known specificity for a given antigen. It is preferred that the host cells not be constitutively capable of making undetermined antibody, but rather that if they are to produce antibody that it be by transformation with DNA encoding a known immunoglobulin. Such immunoglobulins (which may include both heavy as well as light chains) exhibit specificity for a known antigen. Alternatively, these companion immunoglobulin chains will be devoid of functional variable or hypervariable domains (so as to be capable of multimer assembly but not antigen binding activity). For example, a product MSP fusion secreted and recoverable from host cells capable of expressing an intact heavy and light chain companion immunoglobulin will bear an antigen binding functionality as well as an MSP functionality. Such products will facilitate the crosslinking of MSP ligand with any desired antigen. Host cells may make more than one immunoglobulin product in such multiple transformations, and accordingly it may be necessary to recover one multimer form from another. This, however, will be a routine matter requiring separation on a gel or other chromatographic procedure, or by affinity chromatography based on the MSP ligand, the antigen or both.

**[0046]** Other proteins having extended plasma half life are fused to the MSP in similar fashion, except that instead of an immunoglobulin chain a transferrin, albumin, apolipoprotein or other sequence is employed. Monofusions are preferred when MSP chains are fused to single chain plasma proteins which do not ordinarily assemble into multimers.

**[0047]** The boundary for an MSP extracellular domain generally is at, or within about 20 residues N-terminal from, the N-terminus of the membrane anchor domain, and are readily identified from an inspection of the MSP sequence. It is not necessary to use the entire MSP extracellular domain, however, since smaller segments are commonly found to be adequate for ligand binding. Such segments are routinely identified by making deletional mutants or enzymatic digests and screening for ligand binding to identify active fragments, and fall within the scope of the term "MSP".

**[0048]** The MSP extracellular domain generally is fused at its C-terminus to the N-terminus of the immunoglobulin constant region or other stable plasma protein. The precise site at which the fusion is made is not critical; other sites neighboring or within the extracellular region or C-terminal to the mature N-terminus of the plasma protein may be selected in order to optimize the secretion or binding characteristics of the soluble MSP. The optimal site will be determined by routine experimentation.

**[0049]** Exemplary hetero- and chimeric MSP-immunoglobulin variants produced in accordance with this invention are schematically diagrammed below. "A" means at least a portion of the extracellular domain of an MSP containing its ligand binding site; A<sub>1</sub>, A<sub>2</sub>, A<sub>3</sub>, etc. represent individual subunit chains of A; V<sub>L</sub>, V<sub>H</sub>, C<sub>L</sub> and C<sub>H</sub> represent light or heavy chain variable or constant domains of an immunoglobulin; n is an integer; and Y designates a covalent cross-linking moiety.

(a) AC<sub>L</sub>;

(b) AC<sub>L</sub>-AC<sub>L</sub>;

(c) AC<sub>H</sub>-[AC<sub>H</sub>, AC<sub>L</sub>-AC<sub>H</sub>, AC<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>, V<sub>L</sub>C<sub>L</sub>-AC<sub>H</sub>, or V<sub>L</sub>C<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>];

(d) AC<sub>L</sub>-AC<sub>H</sub>-[AC<sub>H</sub>, AC<sub>L</sub>-AC<sub>H</sub>, AC<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>, V<sub>L</sub>C<sub>L</sub>-AC<sub>H</sub>, or V<sub>L</sub>C<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>];

(e) AC<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>-[AC<sub>H</sub>, AC<sub>L</sub>-AC<sub>H</sub>, AC<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>, V<sub>L</sub>C<sub>L</sub>-AC<sub>H</sub>, or V<sub>L</sub>C<sub>L</sub>-V<sub>H</sub>C<sub>H</sub>];

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(f)  $V_L C_L - A C_H - [A C_H, A C_L - A C_H, A C_L - V_H C_H, V_L C_L - A C_H, \text{ or } V_L C_L - V_H C_H]$ ; or

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(g)  $[A - Y]_n - [V_L C_L - V_H C_H]_2$ .

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**[0050]** The structures shown in this table show only key features, e. g. they do not show disulfide bonds. These are omitted in the interests of brevity. However, where such domains are required for binding activity they shall be construed as being present in the ordinary locations which they occupy in the immunoglobulin domain. These examples are representative of divalent antibodies; more complex structures would result by employing immunoglobulin heavy chain sequences from other classes, e.g. IgM. The immunoglobulin  $V_L V_H$  antibody combining site, also designated as the companion immunoglobulin, preferably is capable of binding to a predetermined antigen.

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**[0051]** Exemplary immunoglobulin constructs are described schematically below. Vertical lines indicate a noncovalent or covalent associative relationship.

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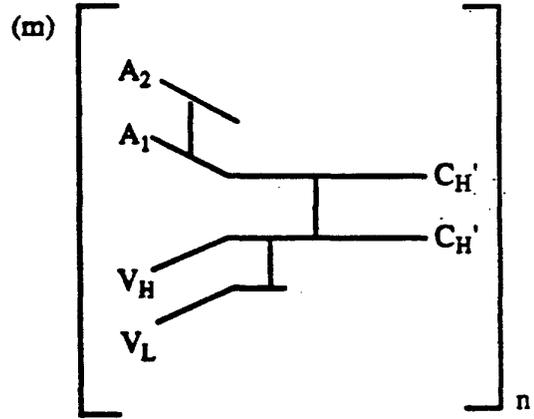
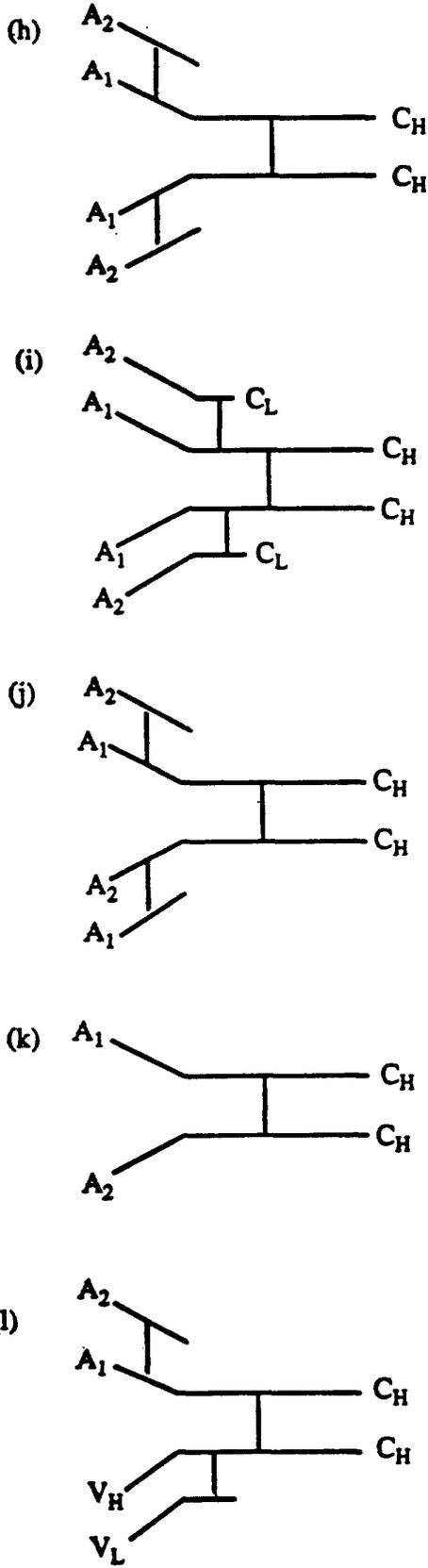
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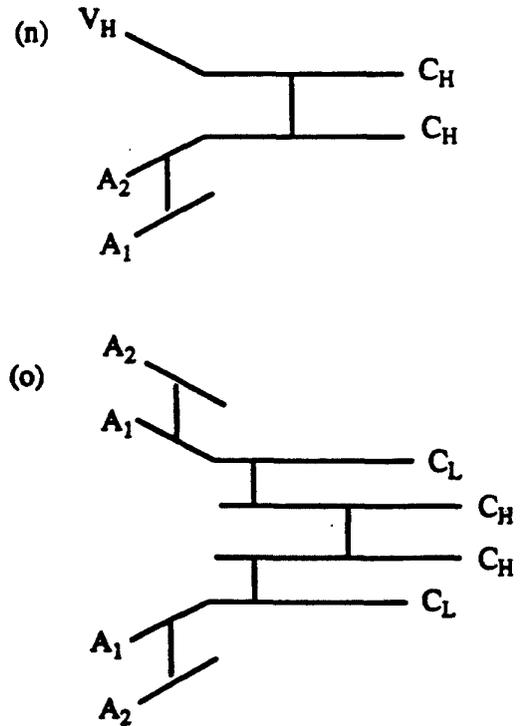
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55



where n = 5 and C<sub>H'</sub> is the secreted heavy chain of IgM



[0052] In product "(o)" the C<sub>H</sub> V domains have been deleted.

[0053] Suitable companion immunoglobulin combining sites and fusion partners are obtained from human IgG-1, -2,

-3, or -4 subtypes, IgA, IgE, IgD or IgM, but preferably IgG-1. It is preferred to use the soluble form of IgM, or one in which the IgM membrane anchor domain has been modified so that it no longer lodges in the membrane.

**[0054]** A preferred embodiment is a fusion of an N-terminal portion of an MSP with a sequence beginning in the hinge region just upstream of the papain cleavage site which defines IgG F<sub>c</sub> chemically (residue 216, taking the first residue of heavy chain constant region to be 114 [Kabat *et al.*, "Sequences of Proteins of Immunological Interest" 4th Ed., 1987], or analogous sites of other immunoglobulins).

**[0055]** The immunoglobulin or other plasma-stable polypeptide is fused to the C-termini of one or more of the MSP subunits, typically in place of at least one transmembrane and cytoplasmic domain of an MSP chain, although ordinarily only one of the subunits is substituted. In the case of GPIIb-IIIa this would be the beta subunit. The immunoglobulin domain such as a heavy chain also can be associated in normal fashion with a truncated or intact immunoglobulin heavy chain.

**[0056]** Variants in which an MSP extracellular domain is substituted for the variable region of an immunoglobulin chain are believed to exhibit improved *in vivo* plasma half life. These chimeras are constructed in a fashion similar to chimeric antibodies in which a variable domain from an antibody of one species is substituted for the variable domain of another species. See, for example, EP 0 125 023; Munro, Nature 312: (13 December 1984); Neuberger *et al.*, Nature 312: (13 December 1984); Sharon *et al.*, Nature 309: (24 May 1984); Morrison *et al.*, Proc. Natl. Acad. Sci. USA 81: 6851-6855 (1984); Morrison *et al.* Science 229:1202-1207 (1985); and Boulianne *et al.*, Nature 312:643-646 (13 December 1984). The DNA encoding the MSP extracellular domain is cleaved by a restriction enzyme at or proximal to the 3' end of the DNA encoding the domain and at a point at or near the DNA encoding the N-terminal end of the mature MSP polypeptide (where use of a different leader is contemplated) or at or proximal to the N-terminal coding region for the MSP (where the native MSP signal is employed). This DNA fragment then is readily inserted into DNA encoding e.g. an immunoglobulin light or heavy chain constant region and, if necessary, tailored by deletional mutagenesis. Preferably, this is a human immunoglobulin. DNA encoding immunoglobulin light or heavy chain constant regions is known or readily available from cDNA libraries or is synthesized. See for example, Adams *et al.*, Biochemistry 19:2711-2719 (1980); Gough *et al.*, Biochemistry 19:2702-2710 (1980); Dolby *et al.*, P.N.A.S. USA, 77:6027-6031 (1980); Rice *et al.*, P.N.A.S. USA 79:7862-7865 (1982); Falkner *et al.*, Nature 298:286-288 (1982); and Morrison *et al.*, Ann. Rev. Immunol. 2:239-256 (1984).

**[0057]** DNA encoding the chimeric chain(s) is transfected into a host cell for expression. If the host cell is producing an immunoglobulin prior to transfection then one need only transfect with the MSP fused to light or to heavy chain to produce a heteroantibody. The aforementioned immunoglobulins having one or more arms bearing the MSP domain and one or more arms bearing companion variable regions result in dual specificity for MSP ligand and for an antigen. These are produced by the above-described recombinant methods or by *in vitro* procedures. In the latter case, for example, F(ab')<sub>2</sub> fragments of the MSP fusion and an immunoglobulin are prepared, the F(ab')<sub>2</sub> fragments converted to Fab' fragments by reduction under mild reducing conditions, and then reoxidized in each other's presence under acidic conditions in accord with methods known *per se*. See also U.S. Patent 4,444,878.

**[0058]** Additionally, procedures are known for producing intact heteroantibodies from immunoglobulins having different specificities. These procedures are adopted for the *in vitro* production of heterochimeric antibodies by simply substituting the MSP fusions for one of the previously employed immunoglobulins.

**[0059]** In an alternative method for producing a heterofunctional antibody, host cells producing an MSP-immunoglobulin fusion, e.g. transfected myelomas, also are fused with B cells or hybridomas which secrete antibody having the desired companion specificity for an antigen. Heterobifunctional antibody is recovered from the culture medium of such hybridomas, and thus may be produced somewhat more conveniently than by conventional *in vitro* resorting methods (EP 68,763).

**[0060]** Another class of MSP variants are deletional variants. Deletions are characterized by the removal of one or more amino acid residues from an MSP sequence. Typically, the membrane anchor and cytoplasmic domains of all MSP subunits are deleted. However, any other suitable site N-terminal to the transmembrane which preserves the matrix protein or ligand-binding capability of the MSP is suitable. Excluded from the scope of deletional variants are the protein digestion fragments that may have heretofore been obtained in the course of elucidating amino acid sequences of MSPs.

**[0061]** Substitutional variants are those in which at least one residue in the MSP sequence has been removed and a different residue inserted in its place. Table 1 below describes substitutions which in general will result in fine modulation of the characteristics of an MSP.

TABLE 1

Original Residue	Exemplary Substitutions
Ala	ser

TABLE 1 (continued)

Original Residue	Exemplary Substitutions
Arg	lys
Asn	gln; his
Asp	glu
Cys	ser; ala
Gln	asn
Glu	asp
Gly	pro
His	asn; gln
Ile	leu; val
Leu	ile; val
Lys	arg; gln; glu
Met	leu; ile
Phe	met; leu; tyr
Ser	thr
Thr	ser
Trp	tyr
Tyr	trp; phe
Val	ile; leu

25 **[0062]** Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in MSP properties will be those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteinyl or prolyl is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanyl, is substituted for (or by) one not having a side chain, e.g., glycyl.

35 **[0063]** A preferred class of substitutional or deletional variants are those involving a membrane anchor region of the MSP. Transmembrane regions of MSP subunits are highly hydrophobic or lipophilic domains that are the proper size to span the lipid bilayer of the cellular membrane. They are believed to anchor the MSP in the cell membrane. Other cell surface molecules are anchored by lipid modification, as by phospholipid anchors.

40 **[0064]** Deletion or substitution of the membrane anchor domain will facilitate recovery and provide a soluble form of the MSP by reducing its cellular or membrane lipid affinity and improving its water solubility. If the membrane anchor domains are deleted one avoids the introduction of potentially immunogenic epitopes, either by exposure of otherwise intracellular polypeptides that might be recognized by the body as foreign or by insertion of heterologous polypeptides that are potentially immunogenic. A principal advantage of the membrane anchor domain-deleted MSP is that it is secreted into the culture medium of recombinant hosts. This variant is soluble in body fluids such as blood and does not have an appreciable affinity for cell membrane lipids, thus considerably simplifying its recovery from recombinant cell culture. Surprisingly, MSPs in which membrane inserted chains have been modified so as to be no longer capable of stable insertion into cell membranes are capable of proper association and secretion from recombinant host cells even if the MSP chains are not fused to a multimer-forming sequence such as an immunoglobulin. A multimer-forming sequence is a multichain polypeptide that contains that portion of a multiple chain polypeptide that, when in the unfused form in nature, forms covalently or noncovalently associated multiple chain structures.

50 **[0065]** It will be amply apparent from the foregoing discussion that substitutions, deletions, insertions or any combination thereof are introduced to arrive at a final construct. None of the variants will have a functional membrane anchor domain and preferably will not have a functional cytoplasmic sequence. This is generally accomplished by deletion of the relevant domain, although adequate insertional or substitutional variants also are effective for this purpose. For example, the transmembrane domain is substituted by any amino acid sequence, e.g. a random or predetermined sequence of about 5 to 50 serine, threonine, lysine, arginine, glutamine, aspartic acid and like hydrophilic residues, which altogether exhibit a hydrophilic hydrophathy profile. Like the deletional (truncated) MSPs, these variants are secreted into the culture medium of recombinant hosts.

**[0066]** MSP variants are prepared conveniently by site specific mutagenesis of nucleotides in the DNA encoding the MSP, thereby producing DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture. Obviously, changes in the DNA encoding the variant MSPs must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure deleterious to expression (EP 75,444A). The MSP variants typically exhibit the same matrix or ligand binding activity as does the naturally-occurring prototype, although variants also are selected in order to modify the characteristics of the MSP as indicated above.

**[0067]** While the site for introducing an amino acid sequence variation is predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random or saturation mutagenesis (where all 20 possible residues are inserted) may be conducted at the target codon or region and the expressed MSP variants screened for the optimal combination of desired activities.

**[0068]** MSP variants that are not capable of binding to their matrix proteins or ligands are useful nonetheless as immunogens for raising antibodies to the MSP or as immunoassay kit components (labelled, as a competitive reagent for native MSP, or unlabelled as a standard for an MSP assay) so long as at least one MSP epitope remains active.

**[0069]** Contemplated herein are MSPs or MSP amino acid sequence or glycosylation variants (including those already described above) wherein one or more MSP subunits are conjugated with a nonproteinaceous polymer. It will be understood that the nonproteinaceous polymer which is conjugated to MSP excludes oligosaccharides that are present in the same positions in the native or starting MSP, i.e. the polymer is extraneous or heterologous to the MSP.

**[0070]** It is within the scope hereof to move, add or delete glycosylation sites by site-directed mutagenesis of MSP polypeptide in order to increase the number of or change the location of the carbohydrate substituents. The nature of the carbohydrate is modified in conventional fashion by *in vitro* enzymatic digestion or by selecting host cells that affix the selected carbohydrate (or do not glycosylate at all).

**[0071]** The nonproteinaceous polymer ordinarily is a hydrophilic synthetic polymer, i.e., a polymer not otherwise found in nature. However, polymers which exist in nature and are produced by recombinant or methods are useful, as are polymers which are isolated from nature. Hydrophilic polyvinyl polymers fall within the scope of this invention, e.g. polyvinylalcohol and polyvinylpyrrolidone. Particularly useful are polyalkylene ethers such as polyethylene glycol, polypropylene glycol, polyoxyethylene esters or methoxy polyethylene glycol; polyoxyalkylenes such as polyoxyethylene, polyoxypropylene, and block copolymers of polyoxyethylene and polyoxypropylene (Pluronic); polymethacrylates; carbomers; branched or unbranched polysaccharides which comprise the saccharide monomers D-mannose, D- and L-galactose, fucose, fructose, D-xylose, L-arabinose, D-glucuronic acid, sialic acid, D-galacturonic acid, D-mannuronic acid (e.g. polymannuronic acid, or alginic acid), D-glucosamine, D-galactosamine, D-glucose and neuraminic acid including homopolysaccharides and heteropolysaccharides such as lactose, amylopectin, starch, hydroxyethyl starch, amylose, dextran sulfate, dextran, dextrans, glycogen, or the polysaccharide subunit of acid mucopolysaccharides, e.g. hyaluronic acid; polymers of sugar alcohols such as polysorbitol and polymannitol; and heparin. Where the polysaccharide is the native glycosylation or the glycosylation attendant on recombinant expression of MSP, the site of substitution ordinarily is located at other than an N or O-linked glycosylation site of the MSP or the MSP variant is an amino acid sequence variant in which an additional or substitute N or O-linked site has been introduced into the molecule.

**[0072]** Mixtures of such polymers are employed, or the polymer may be homogeneous. The polymer prior to crosslinking need not be, but preferably is, water soluble, but the final conjugate must be soluble in biological fluids such as blood. In addition, for therapeutic uses the polymer should not be highly immunogenic when conjugated to the MSP, nor should it possess viscosity that is incompatible with intravenous infusion or injection if it is intended to be administered by such routes.

**[0073]** Preferably the polymer contains only a single group which is reactive with MSP. This helps to avoid crosslinking of MSP molecules. However, it is within the scope herein to optimize reaction conditions to reduce cross-linking, or to purify the reaction products through gel filtration or chromatographic sieves to recover substantially homogeneous derivatives.

**[0074]** The molecular weight of the polymer ranges about from 100 to 500,000, and preferably is about from 1,000 to 20,000. The molecular weight chosen will depend upon the nature of the polymer and the degree of substitution. In general, the greater the hydrophilicity of the polymer and the greater the degree of substitution, the lower the molecular weight that can be employed. Optimal molecular weights will be determined by routine experimentation. Ordinarily, the molecular weight of the MSP-polymer conjugate will exceed about 70,000 although molecules having lesser molecular weights are suitable.

**[0075]** The polymer generally is covalently linked to MSP through a multifunctional crosslinking agent which reacts with the polymer and one or more amino acid or sugar residues of MSP. However, it is within the scope of this invention to directly crosslink the polymer to the MSP by reacting a derivatized polymer with MSP, or vice versa.

**[0076]** A suitable MSP covalent crosslinking site is the N-terminal amino group and epsilon amino groups found on lysine residues, although other amino, imino, carboxyl, sulfhydryl, hydroxyl or other hydrophilic groups serve as useful

sites of substitution. The polymer may be covalently bonded directly to MSP without the use of a multifunctional (ordinarily bifunctional) crosslinking agent. Examples of such crosslinking agents include 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example esters with 4-azidosalicylic acid, homobifunctional imidoesters including disuccinimidyl esters such as 3,3'-dithiobis (succinimidyl-propionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azido-phenyl)dithio] propionimide yield photoactivatable intermediates which are capable of forming cross-links in the presence of light. Alternatively, reactive water soluble matrices such as cyanogen bromide activated carbohydrates and the systems described in U.S. patents 3,959,080; 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; 4,055,635 and 4,330,440 are suitably modified for cross-linking the polymer and MSP. Covalent bonding to MSP amino groups is accomplished by known chemistries based upon cyanuric chloride, carbonyl diimidazole, aldehyde reactive groups (PEG alkoxide plus diethyl acetal of bromoacetaldehyde; PEG plus DMSO and acetic anhydride, or PEG chloride plus the phenoxide of 4-hydroxybenzaldehyde, succinimidyl active esters, activated dithiocarbonate PEG, 2,4,5-trichlorophenylchloroformate or p-nitrophenylchloroformate activated PEG. Carboxyl groups are derivatized by coupling PEG-amine using carbodiimide.

**[0077]** Polymers are conjugated to the oligosaccharide substituents by chemical, e.g. metaperiodate, or enzymatic oxidation, e.g. glucose or galactose oxidase, (to produce the aldehyde derivative of the carbohydrate), followed by reaction with hydrazide or amino-derivatized polymers, in the same fashion as is described by Heitzmann *et al.*, P.N. A.S., 71:3537-3541 (1974) or Bayer *et al.*, Methods in Enzymology, 62:310 (1979), for the labeling of oligosaccharides with biotin or avidin. Further, other chemical or enzymatic methods which have been used heretofore to link oligosaccharides and polymers may be suitable. Substituted oligosaccharides are particularly advantageous since there are fewer carbohydrate substitutions than amino acid sites for derivatization, thus improving the stability, activity and homogeneity of the conjugate. Finally, the MSP oligosaccharide substituents are enzymatically modified to remove sugars, e.g. by neuraminidase digestion, as a final product or prior to polymer derivatization.

**[0078]** The polymer will bear a group which is directly reactive with an amino acid side chain, or the N- or C- terminus of MSP, or which is reactive with the multifunctional cross-linking agent. In general, polymers bearing such reactive groups are known for the preparation of immobilized proteins. In order to use such chemistries here, one should employ a water soluble polymer otherwise derivatized in the same fashion as insoluble polymers heretofore employed for protein immobilization. Cyanogen bromide activation is a particularly useful procedure to employ in crosslinking polysaccharides to MSP.

**[0079]** "Water soluble" in reference to the starting polymer means that the polymer or its reactive intermediate used for conjugation is sufficiently water soluble to participate in a derivatization reaction with MSP.

**[0080]** The degree of substitution of MSP will vary depending upon the number of reactive sites on the protein, whether intact or truncated MSP is used, whether the MSP is a fusion with a protein heterologous to MSP, the molecular weight, hydrophilicity and other characteristics of the polymer, and the particular sites chosen. In general, the MSP portion of the conjugate is substituted with about from 1 to 10 polymer molecules, while any heterologous sequence which is fused to MSP may be substituted with an essentially unlimited number of polymer molecules so long as the activity of the MSP moiety is not significantly adversely affected. The optimal degree of crosslinking is easily determined by an experimental matrix in which the time, temperature and other reaction conditions are varied to change the degree of substitution, after which the ability of the conjugates to bind matrix protein or ligand is determined.

**[0081]** The polymer, e.g., PEG is crosslinked to MSP by a wide variety of methods known *per se* for the covalent modification of proteins with nonproteinaceous polymers such as PEG. Certain of these methods, however, are not preferred for the purposes herein. Cyanuric chloride chemistry leads to many side reactions, including protein cross-linking. In addition, it may be particularly likely to lead to inactivation of proteins containing sulfhydryl groups. Carbonyl diimidazole chemistry (Beauchamp *et al.*, "Anal. Biochem." 131:25-33 [1983]) requires high pH (>8.5), which can inactivate proteins. Moreover, since the "activated PEG" intermediate can react with water, a very large molar excess of "activated PEG" over protein is required. In general, aldehyde chemistry (Royer, U.S. Patent 4,002,531) is preferred since it requires only a 40 fold molar excess of PEG and a 1-2 hr incubation. However, the manganese dioxide suggested by Royer for preparation of the PEG aldehyde is problematic "because of the pronounced tendency of PEG to form complexes with metal-based oxidizing agents" (Harris *et al.*, "J. Polym. Sci., Polym. Chem. Ed." 22:341-352 [1984]). Use of a Moffatt oxidation, utilizing DMSO and acetic anhydride, obviates this problem. In addition, the sodium borohydride suggested by Royer must be used at a high pH and has a significant tendency to reduce disulphide bonds. In contrast, sodium cyanoborohydride, which is effective at neutral pH, has very little tendency to reduce disulphide bonds.

**[0082]** The MSP conjugates of this invention typically are separated from unreacted starting materials by gel filtration. Most conveniently, MSP conjugates are eluted from hydrophobic interaction chromatography medium, e.g. alkyl Sepharose, by the use of a decreasing salt gradient. This, as well as the gel filtration approach described above, resolves conjugates on the basis of the degree of substitution.

**[0083]** The DNA encoding an MSP is obtained by known procedures, in most instances by reference to publications describing DNA encoding the MSP. In general, prokaryotes are used for cloning of MSP variant DNA sequences. For

example, a -resistant strain of *E. coli* JM 101 for propagating M13 phage; Messing *et al.*, Nucl. Acids. Res. 9(2):309-321 [1981]; and *E. coli* K12 strain 294 (ATCC No. 31446) are particularly useful. Other microbial strains which may be used include *E. coli* B, or UM101. These examples are illustrative rather than limiting. Nucleic acid also is cloned using various well known *in vitro* amplification processes.

5 **[0084]** DNA encoding the variant MSPs are inserted for expression into vectors containing promoters and control sequences which are derived from species compatible with the intended host cell. The vector ordinarily, but need not, carry a replication site as well as one or more marker sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using a derivative of pBR322 which is a plasmid derived from an *E. coli* species (Bolivar, *et al.*, Gene 2: 95 [1977]). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid must also contain or be modified to contain promoters and other control elements commonly used in recombinant DNA constructions.

10 **[0085]** Promoters suitable for use with prokaryotic hosts illustratively include the  $\beta$ -lactamase and lactose promoter systems (Chang *et al.*, Nature, 275: 615 [1978]; and Goeddel *et al.*, Nature 281: 544 [1979]), alkaline phosphatase, the tryptophan (trp) promoter system (Goeddel, Nucleic Acids Res. 8: 4057 [1980] and EPO Appln. Publ. No. 36,776) and hybrid promoters such as the tac promoter (H. de Boer *et al.*, Proc. Natl. Acad. Sci. USA 80: 21-25 [1983]). However, other functional bacterial promoters are suitable. Their nucleotide sequences are generally known, thereby enabling a skilled worker operably to ligate them to DNA encoding the MSP variant using linkers or adaptors to supply any required restriction sites (Siebenlist *et al.*, Cell 20: 269 [1980]). Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the antigen.

20 **[0086]** In addition to prokaryotes, eukaryotic microbes such as yeast cultures also are useful as cloning or expression hosts. *Saccharomyces cerevisiae*, or common baker's yeast is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. For expression in *Saccharomyces*, the plasmid YRp7, for example, (Stinchcomb, *et al.*, Nature 282: 39 [1979]; Kingsman *et al.*, Gene 7: 141 [1979]; Tschemper *et al.*, Gene 10: 157 [1980]) is commonly used. This plasmid already contains the trp1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC no. 44076 or PEP4-1 (Jones, Genetics 85: 12 [1977]). The presence of the trp1 lesion as a characteristic of the yeast host cell genome then provides an effective means of selection by growth in the absence of tryptophan.

25 **[0087]** Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.*, J. Biol. Chem. 255: 2073 [1980]) or other glycolytic enzymes (Hess *et al.*, J. Adv. Enzyme Reg. 7: 149 [1968]; and Holland, Biochemistry 17: 4900 [1978]), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

30 **[0088]** Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman *et al.*, European Patent Publication No. 73,657A. Yeast enhancers also are advantageously used with yeast promoters.

35 **[0089]** Promoters for controlling transcription from vectors in mammalian host cells may be obtained from various sources, for example, the genomes of viruses such as polyoma, Simian Virus 40 (SV40), adenovirus, retroviruses, hepatitis-B virus and most preferably cytomegalovirus, or from heterologous mammalian promoters, e.g. the beta actin promoter. The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment which also contains the SV40 viral origin of replication. Fiers *et al.*, Nature, 273: 113 (1978). The immediate early promoter of the human cytomegalovirus is conveniently obtained as a *Hind*III E restriction fragment. Greenaway, P.J. *et al.*, Gene 18: 355-360 (1982). Of course, promoters from the host cell or related species also are useful.

40 **[0090]** DNA transcription in higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually from about 10 to 300bp, that act to increase the transcription initiation capability of a promoter. Enhancers are relatively orientation and position independent having been found 5' (Laimins, L. *et al.*, Proc. Natl. Acad. Sci. 78: 993 [1981]) and 3' (Lusky, M.L., *et al.*, Mol. Cell Bio. 3: 1108 [1983]) to the transcription unit, within an intron (Banerji, J.L. *et al.*, Cell 33: 729 [1983]) as well as within the coding sequence itself (Osborne, T. F., *et al.*, Mol. Cell Bio. 4: 1293 [1984]). Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

45 **[0091]** Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human or nucleated cells) may also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA encoding the MSP.

**[0092]** Expression vector systems generally will contain a selection gene, also termed a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR), thymidine kinase or neomycin. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow independent of a supplemented medium. Two examples are: CHO DHFR<sup>-</sup> cells and mouse LTK<sup>-</sup> cells. These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented medium. An alternative to supplementing the medium is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the DHFR or TK gene will not be capable of survival in non supplemented media.

**[0093]** The second category is dominant selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would survive the selection. Examples of such dominant selection use the drugs neomycin, Southern P. and Berg, P., *J. Molec. Appl. Genet.* **1**: 327 (1982), mycophenolic acid, Mulligan, R.C. and Berg, P. *Science* **209**: 1422 (1980) or hygromycin, Sugden, B. *et al.*, *Mol. Cell. Biol.* **5**: 410-413 (1985). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid) or hygromycin, respectively.

**[0094]** "Amplification" refers to the increase or replication of an isolated region within a cell's chromosomal DNA. Amplification is achieved using a selection agent e.g. methotrexate (MTX) which is inactivated by DHFR. Amplification or the making of successive copies of the DHFR gene results in greater amounts of DHFR being produced in the face of greater amounts of MTX. Amplification pressure is applied notwithstanding the presence of endogenous DHFR, by adding ever greater amounts of MTX to the media. Amplification of a desired gene can be achieved by cotransfecting a mammalian host cell with a plasmid having a DNA encoding a desired protein and the DHFR or amplification gene permitting cointegration. One ensures that the cell requires more DHFR, which requirement is met by replication of the selection gene, by selecting only for cells that can grow in the presence of ever-greater MTX concentration. So long as the gene encoding a desired heterologous protein has cointegrated with the selection gene replication of this gene gives rise to replication of the gene encoding the desired protein. The result is that increased copies of the gene, i.e. an amplified gene, encoding the desired heterologous protein express more of the desired heterologous protein.

**[0095]** Preferred host cells for expressing the MSP variants of this invention are mammalian host-vector systems, examples of suitable hosts including: monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293, Graham, F.L. *et al.*, *J. Gen Virol.* **36**: 59 [1977] and 293S cells, either of which are equally satisfactory); baby hamster kidney cells (BHK, ATCC CCL 10); chinese hamster ovary-cells DHFR (CHO, Urlaub and Chasin, *Proc.Natl.Acad.Sci. (USA)* **77**: 4216, [1980]); mouse sertoli cells (TM4, Mather, J.P., *Biol. Reprod.* **23**: 243-251 [1980]); monkey kidney cells (CV1 ATCC CCL 70); african green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51 cells); and TRI cells (Mather, J.P. *et al.*, *Annals N.Y. Acad. Sci.* **383**: 44-68 [1982]).

**[0096]** "Transformation" means introducing DNA into an organism so that the DNA is replicable, either as an extra-chromosomal element or by chromosomal integration. One suitable for transformation of the host cells is the method of Graham, F. and van der Eb, A., *Virology* **52**: 456-457 (1973). However, other methods for introducing DNA into cells such as by nuclear injection or by protoplast fusion may also be used. If prokaryotic cells or cells which contain substantial cell walls are used as hosts, the preferred method of transfection is calcium treatment using calcium chloride as described by Cohen, F.N. *et al.*, *Proc. Natl. Acad. Sci. (USA)*, **69**: 2110(1972).

**[0097]** Construction of suitable vectors containing the desired coding and control sequences employ standard and manipulative ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to form the plasmids required. Suitable procedures are well known for the construction described herein. See, for example, (Maniatis, T. *et al.*, *Molecular Cloning*, 133-134 Cold Spring Harbor, [1982]; "Current Protocols in Molecular Biology", edited by Ausubel *et al.*, [1987], pub. by Greene Publishing Associates & Wiley-Interscience).

**[0098]** Ordinarily, DNA encoding each subunit of a given MSP (or transmembrane modified variant) is simultaneously cotransfected into the host cell, although such transfections can be done sequentially. MSP variants in which one subunit is exchanged for the analogous subunit of another MSP (to produce heterologous heterodimers) are produced by cotransforming a recombinant host (typically mammalian cell) with each of the heterologous subunits, for example, exchanging the fibronectin  $\alpha$  subunit for the  $\alpha$  subunit of GPIIb-IIIa (an  $\alpha$  subunit exchange), or the fibronectin  $\beta$  subunit for the  $\beta$  subunit of GPIIb-IIIa (a  $\beta$  subunit exchange).

**[0099]** Correct plasmid sequences are confirmed by transforming *E. coli* K12 strain 294 (ATCC 31446) with ligation mixtures, successful transformants selected by ampicillin or tetracycline resistance where appropriate, plasmids from

the transformants prepared, and then analyzed by restriction enzyme digestion and/or sequenced by the method of Messing *et al.*, *Nucleic Acids Res.* 9: 309 (1981) or by the method of Maxam *et al.*, *Methods in Enzymology* 65: 499 (1980).

**[0100]** Host cells are transformed with the expression vectors of this invention. Thereafter they are cultured in appropriate culture media, e.g. containing substances for inducing promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. For expression of GPIIb-IIIa it is preferable that the culture medium contain calcium and magnesium salts since divalent cations are needed to enhance the stability of secreted GPIIb-IIIa and other calcium dependent MSPs.

**[0101]** The secreted MSP variants are recovered and purified from the culture supernatants or lysates of recombinant hosts. Typically, the supernatants are concentrated by ultrafiltration, contacted with a ligand (e.g. RGD) or matrix protein affinity or immunoaffinity resin so as to adsorb the MSP variant, and eluted from the adsorbent. Optionally, the MSP is purified by HPLC, lectin columns, gel exclusion, hydrophobic interaction or ion exchange chromatography.

**[0102]** The purified MSP is formulated into conventional pharmacologically acceptable excipients.

**[0103]** The soluble MSP variants of this invention are useful in therapeutics, diagnostics and preparative procedures. In diagnostics, the soluble MSPs are employed in place of membrane extracts as standards or controls, or are labelled with a radioisotope or other detectable group for use in competitive-type radioimmuno- or radioreceptor assays for the MSP or its antibodies.

**[0104]** The soluble MSPs are crosslinked to insoluble supports by the methods described herein and employed for the purification of their ligands or matrix proteins, e.g. fibronectin, fibrinogen and the like. Alternatively, the soluble MSPs are used to adsorb ligand or matrix protein in solution, followed by precipitation by antisera, ammonium sulfate or the like in order to recover the ligand or matrix protein complex. The complex is then dissociated by HPLC, electrophoresis, gel chromatography or other conventional methods.

**[0105]** Therapeutic uses of soluble MSPs will be a function of the biological activity of each MSP, and will be apparent therefrom. The soluble MSP variants herein may act as agonists or antagonists of the corresponding native, membrane-bound receptors. The soluble GPIIb-IIIa receptor, for example, is useful as an anticoagulant and for the treatment of disorders associated with platelet aggregation, particularly in the prevention of reocclusion following thrombolytic therapy. Soluble matrix receptors, especially soluble GPIIb-IIIa, also are useful as antagonists to matrix-adhesion dependent neoplastic metastasis. Soluble LFA-1 variants are an antagonist of T-lymphocyte function, thereby being efficacious as immunosuppressive or anti-inflammatory agents, particularly in reperfusion injury. Soluble Mac-1 variants may find use in the treatment of complement activation disorders.

**[0106]** In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

**[0107]** "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

**[0108]** "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide or agarose gel to isolate the desired fragment.

**[0109]** "Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the digest on polyacrylamide or agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. This procedure is known generally (Lawn, *R. et al.*, *Nucleic Acids Res.* 9: 6103-6114 [1981], and Goeddel, *D. et al.*, *Nucleic Acids Res.* 8: 4057 [1980]).

**[0110]** "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, *T. et al.*, *Id.* at 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

**[0111]** The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention.

Example 1

Cloning of Glycoprotein IIb (GPIIb) cDNA

5 [0112] Messenger RNA was prepared from cultured human erythroleukemia cells (HEL, ATCC TIB 180). An oligo (dT)-primed cDNA library was prepared using this mRNA in the bacteriophage lambda ZAP (Stratagene Cloning Systems). The lambda ZAP library was screened with a 45-mer oligonucleotide (2b1) derived from the 5' end of the published cDNA sequence for GPIIb from HEL cells (Poncz *et al.*, "J. Biol. Chem." 262(18):8476-8482 [1987]). Several positively-hybridizing phage were purified, and the cDNA inserts they contained were subjected to restriction enzyme digestion analysis. From these results a phage which appeared to contain a full-length coding insert for GPIIb was selected for further analysis. DNA sequencing of this phage insert DNA gave over 300 bases which corresponded exactly with the published cDNA sequence from the 5' end of the mRNA (Poncz *et al.*) except having 4 additional bases on its 5' end. The cDNA insert was digested with *EcoRI* (this site being derived from the linkers ligated to the ends of the cDNAs during production of the library) and *HindIII*, which cuts the GPIIb insert uniquely downstream of the end of the coding sequence. This *EcoRI* to *HindIII* restriction fragment, containing the entire coding region for GPIIb was ligated into mammalian cell expression vector pRK5 (European Appln. Pub. No. 307,247 published 15 March 1989) which had been digested with *EcoRI* and *HindIII*, and expression vector GPIIb-pRK5 was recovered.

Construction of Full-Length Glycoprotein IIIa (GPIIIa) cDNA

20 [0113] A cDNA clone for GPIIIa, incomplete at its 5' end, was obtained (Rosa *et al.*, "Blood" 72(2):593 [1988]). The cDNA was provided as an *EcoRI* (site derived from the cDNA library construction linker) to *PstI* (site downstream of the end of the coding sequence) insert in the plasmid vector pIBI20 (International Biotechnologies, Inc.) This plasmid was digested with *HindIII* to cut the plasmid at the unique *HindIII* site in pIBI20 downstream of the terminal *PstI* site in the cDNA insert, and incompletely with *ApaI*, to give a cDNA fragment bounded by the *ApaI* site at the 5' end of the sequence and *HindIII* from the plasmid vector. The relevant domain for the construction is shown below.

30

```

      -7           -1   I           6
      L   A   G   V   G   V   G   G   P   N   I   C   T
    .... CTG GCG GGC GTT GGC GTA GGA GGG CCC AAC ATC TGT ACC ....
    .... GAC CGC CCG CAA CCG CAT CCT CCC GGG TTG TAG ACA TGG ....
    EcoRI                                     ApaI                                 HindIII
  
```

35 [0114] Synthetic complementary oligonucleotides were used to reconstruct a full-length coding construct for GPIIIa based on the published cloned cDNA sequence (Fitzgerald *et al.*, "J. Biol. Chem." 262(9):3936 [1987]). The oligonucleotide sequence, ending in *ApaI*, was ligated to the *ApaI* site of the above *ApaI-HindIII* fragment, to give a DNA fragment now bounded by *EcoRI* and *HindIII*. This *EcoRI* to *HindIII* fragment, containing the entire coding region for GPIIIa was ligated into pRK5 which had been digested with *EcoRI* and *HindIII*, and expression vector GPIIIa-pRK5 was recovered. The relevant oligonucleotide sequences are shown below.

45

```

      -26
      M   R   A   R   P   R   P   R   P   L   W
    AAT TCT AGA GCC GCC ATG AGA GCA CGT CCT CGA CCA CGT CCT CTC TGG -
      GA TCT CGG CGG TAC TCT CGT GCA GGA GCT GGT GCA GGA GAG ACC -
    EcoRI
    XbaI
  
```

50

```

      A   T   V   L   A   L   G   A   L   A   G   V   G   V   -1   I   P
    GCG ACT GTG CTG GCA CTG GGA GCA CTG GCT GGT GTT GGA GTA GGA GGG CC
    CGC TGA CAC GAC CGT GAC CCT CGT GAC CGA CCA CAA CCT CAT CCT C
      ApaI
  
```

[0115] The synthetic oligonucleotides were designed such that the amino acids encoded were identical to those

predicted from the published cloned cDNAs (Fitzgerald *et al.*, Rosa *et al.*), but the codons were not always identical with the naturally-occurring cloned cDNA. Fig. 3 compares the coding strands of the synthetic and natural sequences. Asterisks between each sequence indicate which nucleotides are identical. These changes were introduced for three reasons.

1. In light of difficulties encountered in sequencing the cDNA, we concluded that the cDNA could contain secondary structure adverse to translational efficiency. To minimize possible secondary structure in the mRNA produced from expression constructs, the percentage of G and C bases in the natural coding sequence was lessened by changing some codons to others which had a lower G and/or C content, but which coded for the same amino acid. These altered codons were chosen such that only codons used frequently in the remainder of the cDNA were substituted. Karnick *et al.*, "J. Biol. Chem." 262(5):9255 (1987); Devlin *et al.*, "Gene" 65:13 (1988).
2. The codon for arginine (R, amino acid -25), immediately following the initiator methionine codon (M -26), was changed from CGA to AGA. Kozak, "Nucl. Acids Res." 15(20):8125 [1987] and Kozak, "J. Mol. Biol." 196:947 [1987].
3. The DNA sequence upstream of the initiator methionine codon was not based on the natural DNA sequence. The synthetic complementary oligonucleotides were such that an *EcoRI* site was present at one end, followed by an *XbaI* recognition sequence, and then followed by a GCC GCC motif immediately upstream of the initiator methionine. Kozak, "J. Mol. Biol." Id.

**[0116]** The plasmids encoding GPIIb and GPIIIa (GPIIb-pRK5 and GPIIIa-pRK5) were transfected in 293S cells and cultured under conventional conditions for transient expression as described below. The cells were harvested and analyzed for GPIIb-IIIa expression. Expression was confirmed by the presence of correctly sized bands on a Western gel, immunologically visualized by FACS sorting, and immunoprecipitation of intact cells labeled metabolically with S<sup>35</sup> or by I<sup>125</sup> surface-labelling.

Example 2

Construction of cDNA Encoding Truncated GPIIb

**[0117]** The starting point for the construction of the GPIIb truncated form was the full-length coding construction for GPIIb described in Example 1. The relevant domain for this construction is shown below.

```

                                     putative transmembrane
                                     region
                                     962
                                     R   A   I
L   R   A   L   E   E
..... CTC CGG GCC TTG GAG GAG AGG GCC ATT .....
..... GAG GCC CGG AAC CTC CTC TCC CGG TAA .....
EcoRI                               StyI

```

The DNA fragment from the *EcoRI* site (upstream of the initiator ATG codon) to the *StyI* site indicated above was isolated and ligated to complementary synthetic oligonucleotides such that the DNA sequence thus obtained coded for the natural GPIIb sequence up to amino acid residue 962 (arginine) and was then followed by a TGA stop codon.

```

A   L   E   E   R   Stop
C TTG GAG GAG AGG TGA TGA A
      CTC CTC TCC ACT ACT TTC GA
StyI                               HindIII

```

**[0118]** In the natural sequence, arginine 962 is followed by an approximately 26 amino acid putative hydrophobic transmembrane domain and a cytoplasmic domain (Poncz *et al.*). Thus, in this construction both of these domains have been deleted from the coding region of the construction. The end of the synthetic fragment terminated in a *HindIII* restriction site. The entire DNA fragment bounded by *EcoRI* and *HindIII* restriction sites was ligated into pRK5 which had been digested with *EcoRI* and *HindIII*. Expression vector GPIIbtrunc-pRK5 was recovered.

**[0119]** The *EcoRI* to *HindIII* fragment outlined above was rescued from GPIIbtrunc-pRK5 and subjected to analysis by DNA sequencing. Over 250 bases from each end of the insert were sequenced and corresponded exactly to that

which was predicted.

#### Construction of cDNA Encoding Truncated GPIIIa

5 [0120] The starting point for the construction of the GPIIIa truncated form was the full-length coding construction for GPIIIa described in Example 1. The relevant domain for this construction is shown below.

10

```

                                     putative transmembrane region
                                     692
                                     P   K   G   P   D   I   L   L
... .. CCC AAG GGC CCT GAC ATC CTG GTG ... ..
... .. GGG TTC CCG GGA CTG TAG GAC CAC ... ..
XbaI           ApaI

```

15 [0121] The DNA fragment from the *XbaI* site (upstream of the initiator ATG codon) to the *ApaI* site indicated below was isolated and ligated to complementary synthetic oligonucleotides such that the DNA sequence thus obtained coded for the natural GPIIIa sequence up to amino acid residue 692 (aspartic acid) and was then followed by a TGA stop codon.

20

```

                                     G   P   D   Stop
                                     CT GAC TGA TGA GAT CTA
CCG GGA CTG ACT ACT CTA GAT TCG A
ApaI                                     HindIII

```

25 [0122] In the natural sequence, aspartic acid 692 is followed by an approximately 29 amino acid putative hydrophobic transmembrane domain and a cytoplasmic domain (Fitzgerald *et al.*) Thus, in this construction both of these domains have been deleted from the coding region of the construction. The end of the synthetic fragment terminated in a *HindIII* restriction site. The entire fragment bounded by *XbaI* and *HindIII* restriction sites, was ligated into pRK5 previously digested with *XbaI* and *HindIII* and trunc expression vector GPIIIatrunc-pRK5 was recovered.

30 [0123] The *XbaI* to *HindIII* fragment outlined above was rescued from GPIIIatrunc-pRK5, and subjected to analysis by DNA sequencing. Over 200 bases from each end of the insert were sequenced and corresponded exactly to that which was predicted.

#### Expression of Truncated Human GPIIb-IIIa Receptor in a Eukaryotic Host

35 [0124] Human embryonic kidney cells (293S) were cotransfected with the expression vectors GPIIbtrunc-pRK5 and GPIIIatrunc-pRK5 using CaPO<sub>4</sub> (Graham *et al.*, "Virology" 52:456 [1973]) using the host system described in EP 260,148.

#### Transient Expression

40 [0125] High levels of transient expression were obtained when 293S cells were cotransfected with GPIIbtrunc-pRK5, GPIIIatrunc-pRK5 and adenovirus VA RNA-DNA (European Appln. Pub. No. 309,237 published 29 March 1989; Akusjarvietal, "Mol. Cell. Biol." 7:549 [1987]) and grown in standard growth media (50% Dulbeccos Modified Eagle Media, 50% F12 mixture, 2 mM L-glutamine and 10% fetal bovine serum). Sixteen hours after glycerol shock cells were transferred to serum free media (Dulbeccos Modified Eagle Media, 0.1% glucose, 10 µg/ml insulin) and grown for a further 48 hours, at which time cells and culture media were harvested. Conditioned cell culture fluid was centrifuged to remove contaminating cell debris and then quick frozen in dry ice-ethanol and stored at -70°C until analyzed. Cells were removed from 6 cm plates by suspension in 0.6 ml of 150 mM NaCl, 10 mM Tris (pH 7.5), 1% Triton X-100, 2 mM PMSF, 0.5 µg/ml leupeptin and 2 µg/ml pepstatin A followed by extraction for 30 minutes on ice with vortexing. Cellular debris was removed by centrifugation at 10,000 g and samples stored at -70°C. The soluble GPIIb-IIIa was recovered by Q-Sepharose (fast-flow) chromatography with 10 column volumes of 20 mM MES buffer/1mM CaCl<sub>2</sub> pH 6.5 and gradient elution over 0-400 mM NaCl. The peak soluble GPIIb-IIIa tended to elute at about 200-250 mM NaCl. The eluate was concentrated to 3% of the column volume of an S-300 column, after which the concentrate was exclusion chromatographed on the a-350 column using 10 mM Tris/150mM NaCl/1mM CaCl<sub>2</sub> pH 7.5. Some of the full length GPIIb

transfected into 293S cells associated with endogenous  $\alpha_v$ . The secretion of soluble GPIIb with soluble GPIIIa avoided the need to purify GPIIb-IIIa from the  $\alpha_v\beta_3$  vitronectin receptor, as would have been the case if the full length subunits had been used. See Bodary *et al.*, *J. Biol. Chem.* 32:18859 (November 15, 1989).

### 5 Stable Expression

[0126] Stable 293S clones expressing truncated GPIIb-IIIa were established by co-transfection of GPIIbtrunc-pRK5 and GPIIIatrunc-pRK5 with pRSVneo (Gorman *et al.*, "Science" 221:551-552 [1983]). Forty eight hours after transfection cells were passaged into standard growth media containing 800  $\mu\text{g/ml}$  of G418. Two weeks later, G418 resistant clones were picked and grown in standard growth media containing 400  $\mu\text{g/ml}$  of G418. Clones were grown for 48 hours in serum free medium and the conditioned culture medium assayed for the expression of secreted forms of GPIIb-IIIa by Western blot analysis.

### 15 Analysis of Expressed Truncated GPIIb-IIIa

[0127] Transiently transfected cells were assayed for expression by pulse-chase analysis followed by immunoprecipitation using a panel of monoclonal antibodies generated against purified platelet GPIIb-IIIa.  $\text{S}^{35}$ -cysteine and -methionine metabolically labeled proteins were recovered from the culture fluid of cells cotransfected with both GPIIbtrunc-pRK5 and GPIIIatrunc-pRK5 as described above. Truncated GPIIb-IIIa was immunoprecipitated from cell culture fluid with a panel of mouse monoclonal antibodies (AP2 [Montgomery *et al.*, "J. Clin. Invest." 71:385 (1983)], 2D2, 3A8, 4B12, and AP3 [Newman *et al.*, "Blood" 65:227 (1985)]) by incubation with Protein A Sepharose CL4B (Pharmacia), bound to rabbit IgG antibodies directed against mouse IgG. Electrophoresis of the immunoprecipitated proteins demonstrated the secretion of recombinant truncated GPIIb-IIIa whose size was in agreement with the molecular weights expected of the modified cDNAs. Monoclonal antibodies specific to the GPIIb-IIIa complex (AP2), GPIIb (2D2, 3A8) and GPIIIa (4B12, AP3) all immunoprecipitate both the GPIIb and GPIIIa truncated proteins, demonstrating that the recombinant secreted proteins are present in the form of a complex. Cells which received no DNA or the GPIIbtrunc-pRK5 alone or GPIIIatrunc-pRK5 alone do not secrete proteins at levels which are detectable by monoclonal antibodies to GPIIb or GPIIIa.

[0128] The expression of individual subunits of GPIIb or GPIIIa in transiently transfected cells was demonstrated using Western blot analysis. Cells were extracted as described above and culture media (recovered as above) were concentrated 2-fold by ultrafiltration and analyzed by electrophoresis on polyacrylamide gels (Laemmli, U.K., "Nature" 227:680-685 [1970]) and by Western Blotting (Towbin *et al.*, *Proc.Natl.Acad.Sci.USA* 76:4350-4354 [1979]). Mouse monoclonal antibodies specific for GPIIb and GPIIIa were used in this analysis. Horse radish peroxidase-conjugated antibodies directed against the murine monoclonals were used to visualize the individual GPIIbtrunc and GPIIIatrunc proteins in the extracts.

[0129] The stable clones expressing the GPIIb-IIIa truncated constructs were shown to secrete the recombinant proteins of the expected sizes using Western blot analysis.

[0130] That the GPIIb-IIIa trunc proteins secreted from stable clones were present as a complex was demonstrated by their detection, after direct transfer of culture medium to nitrocellulose by aspiration, with monoclonal antibody AP2.

[0131] The truncated GPIIb or GPIIIa proteins were not detected in culture media when expressed as individual subunits: either they are not secreted or the efficiency of secretion is reduced to levels which preclude detection by immunoprecipitation or by Western blot analysis.

### 45 Example 3

#### Demonstration of Fibrinogen Binding of Secreted Human GPIIb-IIIa Polypeptide Complex

[0132] The functional activity of the secreted truncated GPIIb-IIIa is shown by its specific absorption to an affinity matrix containing the natural ligand, fibrinogen, for the GPIIb-IIIa receptor.

[0133] A stable clone from Example 2 which was expressing the GPIIb-IIIa truncated polypeptide complex was grown for 20 hours under serum free conditions (DMEM culture medium, 0.1% glucose, 10  $\mu\text{g/ml}$  insulin, 1.5  $\mu\text{g/ml}$  L-cysteine, 2.4  $\mu\text{g/ml}$  L-methionine, 200  $\mu\text{Ci/ml}$   $\text{S}^{35}$  methionine and 200  $\mu\text{Ci/ml}$   $\text{S}^{35}$  cysteine). The conditioned cell culture fluid was first concentrated by ultrafiltration then purified by fibrinogen affinity chromatography. The fibrinogen affinity column was produced by coupling highly purified human fibrinogen to CNBr-activated Sepharose 4B (Pharmacia) using the manufacturer's recommended procedure. The concentrated cell culture fluid was applied first to a control Tris/ethanolamine reacted CNBr-activated Sepharose 4B column and the unbound material applied directly to the fibrinogen-Sepharose column. The contaminating proteins were washed away at room temperature with phosphate buffered saline solution containing 1 mM  $\text{Ca}^{2+}$ , 1mM  $\text{Mg}^{2+}$ , 25 mM octylglucoside (OG) and 2 mM phenylmethylsulfonylfluoride

(PMSF). The bound GPIIb-IIIa was eluted from the column at room temperature with phosphate buffered saline containing 15 mM EDTA, 25 mM OG and 2 mM PMSF. The eluted GPIIb-IIIa was then concentrated by ultrafiltration and the subunits of expected molecular weight identified by autoradiography and by Western blot analysis using monoclonal antibodies specific to GPIIb (3A8) and GPIIIa (4B12). The specificity of the binding to the fibrinogen column is shown by the absence of the protein in the eluate from the control column determined by both methods.

#### Example 4

#### Expression of LFA-1 and Mac-1 truncations

**[0134]** LFA-1 and Mac-1 are integrins having identical beta chains (beta-2) and distinct alpha chains (alpha L and alpha M, respectively). In this study the full length chains were transformed into host cells. In addition, the DNA encoding the transmembrane domains of the alpha and beta chains of each of these integrins was deleted and the truncated DNAs transformed into host cells for coexpression.

**[0135]** Transformants with full length LFA-1 alphaL chain did not express any detectable cell bound alphaL, but cotransformation with truncated alphaL and truncated beta-2, or with truncated alphaM and truncated beta-2, resulted in the secretion of the truncated heterodimers. Interestingly, transformation with the full length alphaM chain of Mac-1 alone did yield cell surface alphaM. It has not been confirmed that this product represents a stable alphaM monomer since it is conceivable that the recombinant alphaM chain became associated with a beta chain endogenous to the host cell.

#### Claims

1. A method for the preparation of a soluble analogue of an integrin comprising an  $\alpha$ -subunit and a  $\beta$ -subunit, comprising:

(1) introducing into the nucleic acid encoding the  $\alpha$ -subunit and the  $\beta$ -subunit of the integrin a mutation which serves to delete or modify the membrane anchor domains thereof such that the mutated nucleic acid encodes an amino acid sequence variant of the integrin which is no longer capable of becoming lodged in a cell membrane,

(2) transforming a host cell with the nucleic acid of step (1),

(3) culturing the host cell of step (2), and

(4) recovering from the host cell culture soluble integrin comprising associated  $\alpha$ - and  $\beta$ -subunits, said integrin being biologically active as demonstrated by its ability to bind a ligand ordinarily bound by the integrin.

2. The method of claim 1 wherein the  $\alpha$ - and  $\beta$ -subunits of the integrin recovered at step (4) are noncovalently associated.

3. The method of claim 1 or claim 2 wherein the membrane anchor domain is a transmembrane domain.

4. The method according to any one of claims 1 to 3 wherein the integrin is a heterodimeric receptor that participates directly in intercellular adhesion or adhesion of cells to extracellular matrix proteins.

5. The method of claim 4 wherein the integrin is a leukocyte adhesion receptor.

6. The method of claim 4 wherein the integrin is a member of the VLA family.

7. The method according to any one of claims 1 to 3 wherein the integrin is GPIIb-IIIa.

8. The method of claim 7 wherein the integrin is GPIIb-IIIa and the recovered GPIIb-IIIa analogue is capable of binding fibrinogen, fibronectin, vitronectin or von Willebrand factor.

9. The method according to any one of claims 1 to 3 wherein the integrin is Mac1.

10. The method according to any one of claims 1 to 3 wherein the integrin is LFA-1.

11. A method according to any one of claims 1 to 3 wherein the integrin is p150,95.

12. The method according to any one of claims 1 to 3 wherein the integrin is capable of binding to polypeptides containing the sequence RGD.
- 5 13. The method according to any one of claims 1 to 3 wherein the integrin comprises a subunit having the consensus N-terminal sequence Tyr/Phe/Leu-Asn-Leu-Asp, requires a divalent cation for ligand binding, or contains an amino acid domain having substantial sequence homology to the calmodulin calcium binding domain.
- 10 14. The method according to any one of claims 1 to 3 wherein the  $\alpha$ -subunit of the integrin contains two disulfide bonded polypeptide chains, only one of which comprises a membrane anchor domain.
- 15 15. The method according to any one of the preceding claims wherein the mutation is the substitution of the membrane anchor domain of at least one of the subunits of the integrin with a hydrophilic amino acid sequence.
16. The method of claim 15 wherein the hydrophilic amino acid sequence comprises an immunoglobulin constant domain.
17. The method of claim 16 wherein the constant domain is a heavy chain constant domain.
- 20 18. The method of claim 16 or 17 wherein the host cell is transformed with nucleic acid encoding:  
(1) a fusion of a first integrin subunit and an immunoglobulin heavy chain constant domain, and  
(2) with nucleic acid encoding a second integrin subunit that is not fused with immunoglobulin, this second integrin subunit being capable of binding directly to the first integrin subunit.
- 25 19. The method according to any one of claims 1 to 11 wherein the mutation comprises amino acid insertion substitution or deletion in the membrane anchor domain of at least one of the subunits of the integrin.
20. The method of claim 17 wherein the membrane anchor domain is deleted.
- 30 21. The method of claim 20 wherein the cytoplasmic domain is deleted.
22. The method according to any one of claims 1 to 11 wherein the mutation comprises insertion of heterologous nucleic acid encoding a polypeptide into the DNA encoding the integrin, wherein the polypeptide lacks a heterologous multimer forming domain.
- 35 23. A secreted amino acid sequence variant of an integrin which is biologically active as demonstrated by its ability to bind to a ligand ordinarily bound by the integrin, the variant comprising naturally associated  $\alpha$ - and  $\beta$ -subunits, wherein the membrane anchor domains of the  $\alpha$ -subunit and the  $\beta$ -subunit of the integrin have been deleted or modified such that the variant is not capable of becoming lodged in a cell membrane and wherein the variant  $\alpha$ - and  $\beta$ -subunits associate naturally and lack immunoglobulin constant domain multimer forming sequences.
- 40 24. A soluble integrin amino acid sequence variant comprising associated  $\alpha$ - and  $\beta$ -subunits which is biologically active as demonstrated by its ability to bind to a ligand ordinarily bound by the integrin and that is not capable of becoming lodged in a cell membrane, wherein the membrane anchor domains of the  $\alpha$ - and  $\beta$ -subunits of the integrin are deleted.
- 45 25. The variant of claim 24 which is free of detergent.
26. The variant of claim 24 or 25 wherein the integrin is GPIIb-IIIa.
- 50 27. The variant of claim 24 or 25 wherein the integrin is LFA-1.
28. The variant of claim 24 or 25 wherein the integrin is Mac-1.
- 55 29. The variant according to any one of claims 24 to 28 wherein the cytoplasmic domains of the  $\alpha$ - and  $\beta$ -subunits of the integrin are deleted.
30. A sterile aqueous solution comprising the variant of any one of claims 23 to 29.

**Patentansprüche**

1. Verfahren zur Herstellung eines löslichen Analogs eines Integrins, das eine  $\alpha$ -Untereinheit und eine  $\beta$ -Untereinheit umfasst, wobei das Verfahren Folgendes umfasst:
  - (1) das Einführen einer Mutation, die zur Deletion oder Modifikation ihrer Membranankerdomänen dient, in die für die  $\alpha$ -Untereinheit und die  $\beta$ -Untereinheit des Integrins kodierende Nucleinsäure, so dass die mutierte Nucleinsäure für eine Aminosäuresequenzvariante des Integrins kodiert, die sich nicht mehr in einer Zellmembran festsetzen kann,
  - (2) das Transformieren einer Wirtszelle mit der Nucleinsäure aus Schritt (1),
  - (3) das Kultivieren der Wirtszelle aus Schritt (2), sowie
  - (4) das Gewinnen von löslichem Integrin aus der Wirtszellenkultur, das assoziierte  $\alpha$ - und  $\beta$ -Untereinheiten umfasst, wobei das Integrin biologisch aktiv ist, was sich durch seine Fähigkeit zur Bindung eines Liganden zeigt, der normalerweise vom Integrin gebunden wird.
2. Verfahren nach Anspruch 1, worin die  $\alpha$ - und  $\beta$ -Untereinheiten des in Schritt (4) gewonnenen Integrins nichtkovalent assoziiert sind.
3. Verfahren nach Anspruch 1 oder 2, worin die Membranankerdomäne eine Transmembrandomäne ist.
4. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin ein heterodimerer Rezeptor ist, der direkt an der interzellulären Adhäsion oder der Adhäsion von Zellen an extrazellulären Matrixproteinen beteiligt ist.
5. Verfahren nach Anspruch 4, worin das Integrin ein Leukozytenadhäsionsrezeptor ist.
6. Verfahren nach Anspruch 4, worin das Integrin ein Mitglied der VLA-Familie ist.
7. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin GPIIb-IIIa ist.
8. Verfahren nach Anspruch 7, worin das Integrin GPIIb-IIIa ist und das gewonnene GPIIb-IIIa-Analog zur Bindung an Fibrinogen, Fibronectin, Vitronectin oder von Willebrand-Faktor fähig ist.
9. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin Mac1 ist.
10. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin LFA-1 ist.
11. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin p150,95 ist.
12. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin zur Bindung an Polypeptide fähig ist, die die Sequenz RGD enthalten.
13. Verfahren nach einem der Ansprüche 1 bis 3, worin das Integrin eine Untereinheit umfasst, die die N-terminale Konsens-Sequenz Tyr/Phe/Leu-Asn-Leu-Asp umfasst, ein zweiwertiges Kation zur Ligandenbindung erfordert oder eine Aminosäuredomäne enthält, die im Wesentlichen Sequenzhomologie mit der Calmodulin-Calciumbindungsdomäne aufweist.
14. Verfahren nach einem der Ansprüche 1 bis 3, worin die  $\alpha$ -Untereinheit des Integrins zwei disulfidgebundene Polypeptidketten enthält, von denen nur eine eine Membranankerdomäne umfasst.
15. Verfahren nach einem der vorangegangenen Ansprüche, worin die Mutation die Substitution der Membranankerdomäne zumindest einer der Untereinheiten des Integrins durch eine hydrophile Aminosäuresequenz ist.
16. Verfahren nach Anspruch 15, worin die hydrophile Aminosäuresequenz eine konstante Domäne eines Immunglobulins umfasst.
17. Verfahren nach Anspruch 16, worin die konstante Domäne eine konstante Schwereketten-Domäne ist.
18. Verfahren nach Anspruch 16 oder 17, worin die Wirtszelle mit Nucleinsäure transformiert wird, die kodiert für:

(1) eine Fusion einer ersten Integrin-Untereinheit und einer konstanten Schwereketten-Domäne eines Immunglobulins, und

(2) mit Nucleinsäure, die für eine zweite Integrin-Untereinheit kodiert, die nicht mit Immunglobulin fusioniert ist, wobei diese zweite Integrin-Untereinheit zur direkten Bindung an die erste Integrin-Untereinheit fähig ist.

- 5
19. Verfahren nach einem der Ansprüche 1 bis 11, worin die Mutation Aminosäure-Insertion, -Substitution oder -Deletion in der Membranankerdomäne zumindest einer der Untereinheiten des Integrins umfasst.
- 10
20. Verfahren nach Anspruch 17, worin die Membranankerdomäne deletiert wird.
21. Verfahren nach Anspruch 20, worin die Cytoplasmadomäne deletiert wird.
- 15
22. Verfahren nach einem der Ansprüche 1 bis 11, worin die Mutation die Insertion heterologer Nucleinsäure, die für ein Polypeptid kodiert, in die DNA umfasst, die für das Integrin kodiert, worin dem Polypeptid eine heterologe Multimer-Bildungsdomäne fehlt.
- 20
23. Sekretierte Aminosäuresequenzvariante eines Integrins, das biologisch aktiv ist, was sich durch seine Fähigkeit zur Bindung eines Liganden zeigt, der normalerweise vom Integrin gebunden wird, wobei die Variante natürlich assoziierte  $\alpha$ - und  $\beta$ -Untereinheiten umfasst, worin die Membranankerdomänen der  $\alpha$ -Untereinheit und der  $\beta$ -Untereinheit des Integrins deletiert oder modifiziert worden sind, so dass die Variante nicht fähig ist, sich in der Zellmembran festzusetzen, und worin die Varianten- $\alpha$ - und - $\beta$ -Untereinheiten natürlich assoziieren und ihnen Konstantdomänen-Multimer-Bildungssequenzen eines Immunglobulins fehlen.
- 25
24. Assoziierte  $\alpha$ - und  $\beta$ -Untereinheiten umfassende, lösliche Integrin-Aminosäuresequenzvariante, die biologisch aktiv ist, was sich durch ihre Fähigkeit zur Bindung eines Liganden zeigt, der normalerweise vom Integrin gebunden wird, und die nicht fähig ist, sich in einer Zellmembran festzusetzen, worin die Membranankerdomänen der  $\alpha$ - und  $\beta$ -Untereinheiten des Integrins deletiert sind.
- 30
25. Variante nach Anspruch 24, die frei von Detergens ist.
26. Variante nach Anspruch 24 oder 25, worin das Integrin GPIIb-IIIa ist.
27. Variante nach Anspruch 24 oder 25, worin das Integrin LFA-1 ist.
- 35
28. Variante nach Anspruch 24 oder 25, worin das Integrin Mac-1 ist.
29. Variante nach einem der Ansprüche 24 bis 28, worin die Cytoplasmadomänen der  $\alpha$ - und  $\beta$ -Untereinheiten des Integrins deletiert sind.
- 40
30. Sterile wässrige Lösung, die eine Variante nach einem der Ansprüche 23 bis 29 umfasst.

### Revendications

- 45
1. Procédé pour la préparation d'un analogue soluble d'une intégrine comprenant une sous-unité  $\alpha$  et une sous-unité  $\beta$ , comprenant les étapes consistant :
- 50
- (1) à introduire dans l'acide nucléique codant pour la sous-unité  $\alpha$  et la sous-unité  $\beta$  de l'intégrine une mutation qui sert à éliminer par délétion ou modifier les domaines d'ancrage aux membranes de cette intégrine de telle sorte que l'acide nucléique muté code pour un variant de séquence d'acides aminés de l'intégrine qui ne soit plus capable de venir se loger dans une membrane cellulaire,
- (2) à transformer une cellule hôte avec l'acide nucléique de l'étape (1),
- (3) à cultiver la cellule hôte de l'étape (2), et
- 55
- (4) à recueillir à partir de la culture de cellules hôtes une intégrine soluble comprenant les sous-unités  $\alpha$  et  $\beta$  associées, ladite intégrine étant biologiquement active de la manière démontrée par son aptitude à fixer un ligand fixé habituellement par l'intégrine.
2. Procédé suivant la revendication 1, dans lequel les sous-unités  $\alpha$  et  $\beta$  de l'intégrine recueillie dans l'étape (4) sont

associées de manière non covalente.

- 5
3. Procédé suivant la revendication 1 ou la revendication 2, dans lequel le domaine d'ancrage aux membranes est un domaine transmembranaire.
- 10
4. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine est un récepteur hétérodimère qui participe directement à l'adhérence intercellulaire ou l'adhérence des cellules aux protéines de la matrice extracellulaire.
- 15
5. Procédé suivant la revendication 4, dans lequel l'intégrine est un récepteur d'adhérence leucocytaire.
6. Procédé suivant la revendication 4, dans lequel l'intégrine est un membre de la famille VLA.
7. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine consiste en GPIIb-IIIa.
- 20
8. Procédé suivant la revendication 7, dans lequel l'intégrine consiste en GPIIb-IIIa et l'analogue de GPIIb-IIIa recueilli est capable de se lier au fibrinogène, à la fibronectine, à la vitronectine ou au facteur de von Willebrand.
9. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine consiste en Mac1.
- 25
10. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine consiste en LFA-1.
11. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine consiste en p150,95.
- 30
12. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine est capable de se lier à des polypeptides contenant la séquence RGD.
13. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel l'intégrine comprend une sous-unité ayant la séquence N-terminale consensus Tyr/Phe/Leu-Asn-Leu-Asp, a besoin d'un cation divalent pour la liaison à un ligand, ou contient un domaine d'acides aminés présentant une homologie de séquence substantielle avec le domaine de liaison de calcium de calmoduline.
- 35
14. Procédé suivant l'une quelconque des revendications 1 à 3, dans lequel la sous-unité  $\alpha$  de l'intégrine contient deux chaînes polypeptidiques réunies par des liaisons disulfure, dont une seule comprend un domaine d'ancrage aux membranes.
- 40
15. Procédé suivant l'une quelconque des revendications précédentes, dans lequel la mutation est la substitution du domaine d'ancrage aux membranes d'au moins l'une des sous-unités de l'intégrine par une séquence d'acides aminés hydrophile.
- 45
16. Procédé suivant la revendication 15, dans lequel la séquence d'acides aminés hydrophile comprend un domaine constant d'immunoglobuline.
17. Procédé suivant la revendication 16, dans lequel le domaine constant est un domaine constant de chaîne lourde.
- 50
18. Procédé suivant la revendication 16 ou 17, dans lequel la cellule hôte est transformée :
- (1) avec un acide nucléique codant pour une fusion d'une première sous-unité d'intégrine et d'un domaine constant de chaîne lourde d'immunoglobuline, et
- (2) avec un acide nucléique codant pour une seconde sous-unité d'intégrine qui n'est pas fusionnée à une immunoglobuline, cette seconde sous-unité d'intégrine étant capable de se lier directement à la première sous-unité d'intégrine.
- 55
19. Procédé suivant l'une quelconque des revendications 1 à 11, dans lequel la mutation comprend une insertion, substitution ou délétion d'acides aminés dans le domaine d'ancrage aux membranes d'au moins une des sous-unités de l'intégrine.
20. Procédé suivant la revendication 17, dans lequel le domaine d'ancrage aux membranes est éliminé par délétion.

21. Procédé suivant la revendication 20, dans lequel le domaine cytoplasmique est éliminé par délétion.

22. Procédé suivant l'une quelconque des revendications 1 à 11, dans lequel la mutation comprend l'insertion d'un acide nucléique hétérologue codant pour un polypeptide dans l'ADN codant pour l'intégrine, ledit polypeptide étant dépourvu de domaine de formation de multimère hétérologue.

23. Variant de séquence d'acides aminés sécrétés d'une intégrine qui est biologiquement actif de la manière démontrée par son aptitude à se lier à un ligand habituellement fixé par l'intégrine, variant qui comprend les sous-unités  $\alpha$  et  $\beta$  naturellement associées, dans lequel les domaines d'ancrage aux membranes de la sous-unité  $\alpha$  et de la sous-unité  $\beta$  de l'intégrine ont été éliminés par délétion ou modifiés, de telle sorte que le variant ne soit pas capable de venir se loger dans une membrane cellulaire, et dans lequel les sous-unités  $\alpha$  et  $\beta$  du variant s'associent naturellement à des, et sont dépourvues de, séquences formant un multimère de domaine constant d'immunoglobuline.

24. Variant de séquence d'acides aminés d'intégrine soluble comprenant les sous-unités  $\alpha$  et  $\beta$  associées, qui est biologiquement actif de la manière démontrée par son aptitude à se lier à un ligand habituellement fixé par l'intégrine et qui n'est pas capable de venir se loger dans une membrane cellulaire, dans lequel les domaines d'ancrage aux membranes des sous-unités  $\alpha$  et  $\beta$  de l'intégrine sont éliminés par délétion.

25. Variant suivant la revendication 24, qui est dépourvu de détergent.

26. Variant suivant la revendication 24 ou 25, dans lequel l'intégrine consiste en GPIIb-IIIa.

27. Variant suivant la revendication 24 ou 25, dans lequel l'intégrine consiste en LFA-1.

28. Variant suivant la revendication 24 ou 25, dans lequel l'intégrine consiste en Mac-1.

29. Variant suivant l'une quelconque des revendications 24 à 28, dans lequel les domaines cytoplasmiques des sous-unités  $\alpha$  et  $\beta$  de l'intégrine sont éliminés par délétion.

30. Solution aqueuse stérile comprenant le variant suivant l'une quelconque des revendications 23 à 29.



Fig. 1(b)

```

        bsrI      styI
        haeIII    pfIMI
        eaeI      sau96I
        cfrI      haeIII
        fnu4HI    bsajI
        mnlI      asuI
        bspI286  bsajI
        bbvI     bsajI
        mnlI     bsajI
        nlaIV    bsajI
        bsmal    bsajI
        301 AGGGGGCCAGTGGCCCTCGCTGCTTTGACCTCCGCTGATGAGACCCCGAATGTAGCTCCCAAACTTTACAACCTTCAAGGCCCCCAGGACTGGG
        TCCCGCGGTACGGGGGACGAGAAACGGAGACTACTGCGGCTTACATCGAGGTTGAATGTTTGAAGTCCGGCGTTCCTGACCC
        62 G G Q C P S L L F D L R D E T R N V G S Q T L Q T F K A R Q G L G
        fnu4HI
        hgaI      hgaI
        ahaII     ahaII
        acyI      acyI
        aluI      aluI
        pvuII     pvuII
        aatII     aatII
        haeIII    haeIII
        hinPI     hinPI
        scrFI     scrFI
        ecorII    ecorII
        bstNI     bstNI
        401 GGCTCGCTCCCTCAGTGGAGCGAGCTCATTTCTGGCTGGCCCTGGCAGCACCTGGAACCTCTAGAAAGACTGAGGAGGCTGAGAAGACGCCCGTA
        CCGCAGCCAGCTCGACCTCGCTGAGTAACCCGGAGCCGGGGACCGTGTGACCTTGCAGATCTTTCTGACTCCCGACCTCTCTGCGGGCAT
        95 A S V V S W S D V I V A C A P W Q H W N V L E K T E E A E K T P V
        fnu4HI
        haeIII    haeIII
        xmaIII    hinPI
        eagI      hhaI
        eaeI      thaI
        cfrI      fnuDII
        notI     fnu4HI
        rsaI     rsaI
        fnu4HI    fnu4HI
        bstUI     bstUI
        scaI     scaI
        501 GGTAGCTGCTTTTGGTCAGCCAGAGCGGCCCGCCGCGAGTACTCCCTCCCTGTCGCCGGAAACACCTGAGCGCAFTTACGTGGAAAATGATTTTA
        CCATCGACGAAAACCGACTCGGTCTCTCGCGCGCGCGGCTCATGAGGGGACAGCGCCCTGTGGACTCGCGTAATGCACCTTTTACTAAAAT
        128 G S C F L A Q P E S G R R A E Y S P C R G N T L S R I Y V E N D F S
        fnu4HI
        ddeI      ddeI
        espI      espI
        fnu4HI    fnu4HI
        ddeI     ddeI
        bsaAI    bsaAI
        aluI      aluI
        601 GCTGGACAAGCGTTACTGTGAGCGGGTTCAGCTCCGTTGCTCAGTCCGTTGCTCAGCCCGGAGAGCTGCTGTTGGGGCTCCTGGCGGTATTTATTTCTAGGTCT
        CGACCTGTTCCCAATGACACTTCCCGGAGTTCGAGCACCCACTGAGTCCGGCTCGACACCAACCCCGGACCGCGGATATAAAGATCCAGA
        162 W D K R Y C E A G F S S V V T Q A G E L V L G A P G G Y F L G L
        fnu4HI
        mspI      mspI
        haeIII    haeIII
        hqiJII    hqiJII
        bspI286  bspI286
        banII    banII
        fnu4HI    fnu4HI
        ddeI     ddeI
        bsmal    bsmal
        701 GCTGGCAAGCGTTCAGTGGAGCGGGTTCAGTCCGTTGCTCAGTCCGTTGCTCAGCCCGGAGAGCTGCTGTTGGGGCTCCTGGCGGTATTTATTTCTAGGTCT
        CGACCTGTTCCCAATGACACTTCCCGGAGTTCGAGCACCCACTGAGTCCGGCTCGACACCAACCCCGGACCGCGGATATAAAGATCCAGA
        195 L A Q A P V A D I F S S Y R P G I L L W H V S S Q S L S F D S S N
        bsajI
        sau96I
        haeIII
        asuI
        scrFI     scrFI
        ecorII    nlaIV
        ecorII    nlaIV
        bstNI     bstNI
        paeR7I   paeR7I
        avai     avai
        bsajI    bsajI
        fokI     fokI
        pmlI     pmlI
        bsaAI    bsaAI
        mnlI     mnlI
        701 CCTGGCCAGGCTCCAGTTCGGATATTTTCTCGAGTACCCCGCCAGGATCCCTTTGTGGCACCGTGTCTCCAGAGCCCTCTCCTTTGACTCCAGCAAC
        GGACCGGTCCGAGTCAACCGCTATAAAGAGCTCAATGGCGGTCCGTAGAAACCCGTGACAGGAGGTTCTCGGAGAGGAACTGAGGTCTGTTG
        195 L A Q A P V A D I F S S Y R P G I L L W H V S S Q S L S F D S S N
    
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Fig. 1(c)

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sau3AI          bsaJI          bsp1286
mboI            haeIII         nlaIV
dpnI            eaeI           hgiCI
xhoII          cfri           bani
bstYI         rsal          aluI
                rsaI          aluI
                cfri           aluI
                taqI           aluI
801 CCAGACTACTCGACGGTACTGGGGTACTCGGTGGCCCTGGCGGAGTTCGACGGGATCTCAACACTACAGAATATGTCTCGTGGTCCCGACTTGG
GGTCTATGAAGCTGCCGATGACCCCAATGAGCCACCGGACCGCTCAAGTGGCCCTAGANNTTGATGTCTTATACAGAGCCACGGGGTGAACCT
228 P E Y F D G Y W G Y S V A V G E F D G D L N T T E Y V V G A P T W S

                hinPI
                thai
                fnuDII
                bstUI
                hinPI
                hhai
                bssHII
                hgaI
                ahaII
                fnu4HI
                bbvI
                mnlI
                alwNI
                sfANI
                bbvI
                hhai
                acyI
                bsmI
                alwNI
901 CCTGGACCCTGGGACCGGTGGAATTTGGATTCCTACTACAGAGGCTGCATCGGCTGGCCGACAGCAGATGGCGTCTGATTTTGGCATTCAGTGGC
CGACTGGGACCCCTGGCACCTTTAAACCTAAGGATGATGCTCCGACGTAGCCGCGCTCTCGTCTACCCGACGATAAAACCCGTAAGTCAACC
262 W T L G A V E I L D S Y Y Q R L H R L R A E Q M A S Y F G H S V A

                scrFI
                hindII
                hincII
                ahaII
                acyI
                aatII
                foki
                mnlI
                dpnI
                haeIII
                hhai
                hinPI
                hhai
                haeIII
                cauII
                bsrI
                scrFI
                nciI
                mspI
                hpaII
                cauII
                bsrI
1001 TCTCACTGACGTCAACGGGATGGGAGCATGATCTGCTGGTGGCGCTCCACTGTATATGGAGAGCCGGGACAGCCGAAACTGGCCGAAGTGGGGCGT
ACAGTACTGACGTGGCCCTACCCCTCCGCTACTAGACGACCCACCCCGGAGGTGACATATACCTCTCGGCCCGTCTGGCTTTGACCCGGTTCACCCCGCA
295 V T D V N G D G R H D L L V G A P L Y M E S R A D R K L A E V G R

                sau96I
                nlaIV
                eco0109I
                hinPI
                thai
                haeIII
                hhai
                fnuDII
                fnu4HI
                mnlI
                fnuDII
                nlaIV
                bbvI
                bstUI
                hgiCI
                bsp1286
                psti
                fnu4HI
                asuI
                pflMI
                mnlI
                bsrI
                aluI
                hinfi
                xcmI
1101 GTGTATTTTCTCTGACCGCGGAGCCCGGAGCCCGGCTGGGTGGCCCGGCTCCCGGCTGGGAGTGGCCGATTCGGCTTGGCCATCG
CACATAAACAAAGGACGTCCGGCTCCGGGGTCCGCGACCCACCGGCTGGAGATACCCGCTAAGCCGAGACGGTAGC
328 V Y L F L Q P R G P H A L G A P S L L L T G T Q L Y G R F G S A I A

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